94350 SEARCH REQUEST FORM

Requestor's Name: Gambel	Serial Number: ロピ/Чピチ2ピラ
Date: 9/6/00 Phone: 308.3	9977 Art Unit: 644
Search Topic: Please write a detailed statement of search topic. Describe specificaterms that may have a special meaning. Give examples or relevent of please attach a copy of the sequence. You may include a copy of the	citations, authors, keywords, etc., if known. For sequences,
182-5/0/n- SCQ + SCQ /ATUR	FORACE SMRUL
363-39+ 919-570-354 9110-29+-301 9111-250-154	10 NO: 1 NO: 12
AA 8-	r Sor Lys Cys
E E	
PRIUST.	
STAFF USE	ONLY
Date completed: 913 00 Search Searcher: Terminal time: " Elapsed time:	M. P

PTO-1590 (9-90)

=> fil reg

FILE 'REGISTRY' ENTERED AT 07:04:18 ON 13 SEP 2000 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT. PLEASE SEE "HELP USAGETERMS" FOR DETAILS. COPYRIGHT (C) 2000 American Chemical Society (ACS)

12 SEP 2000 HIGHEST RN 288839-14-5 STRUCTURE FILE UPDATES: DICTIONARY FILE UPDATES: 12 SEP 2000 HIGHEST RN 288839-14-5

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 11, 2000

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Structure search limits have been increased. See HELP SLIMIT for details.

=> e ksskc/sqep

E1 E2 E3 E4	1 1 0>	KSSKAVAAWTLKAAASGPSNTPPEI/SQEP KSSKAVAAWTLKAAAVNIRNCCYI/SQEP KSSKC/SQEP KSSKESSKKPKENKPLKEEKIVPKMAFKEPKPMSKEPKPDSNLLTITSGQDKKAPSKRPP ISDSEELSAKKRKKSSSEALFKSFSSAPPLILTCSADKKQIKDKSHVKMGKVKIESETSE
E5	1	KKKSTLPPFDDIVDPNDSDVEENISSKSDSEQPSPASSSSSSSSSFTPSQTRQQGPLRSI MKDLHSDDNEEESDEVEDND/SQEP KSSKHRSFLLKKSGGNQVSLYQKWWNSQLKKSLCYSTVAALIFMIPSQESFADSLIDLNL GLDPSVECLSGDGAFSVGYFTKAGSTPVEYQPFKYDVSKKTFTILSVETANQSGYAYGIS
		YDGTITVGTCSLGAGKYNGAKWSADGTLTPLTGITGGTSHTEARAISKDTQVIEGFSYDA SGQPKAVQWASGATTVTQLA/SQEP
E6	1	KSSKHRSFLLKKSGGNQVSLYQKWWNSQLKKSLCYSTVAALIFMIPSQESFADSLIDLNL GLDPSVECLSGDGAFSVGYFTKAGSTPVEYQPFKYDVSKKTFTILSVETANQSGYAYGIS YDGTITVGTCSLGAGKYNGAKWSADGTLTPLTGITGGTSHTEARAISKDTQVIEGFSYDA SGOPKAVOWASGGLQ/SQEP
E7	1	KSSKKPRKRTTHKRK/SQEP
E8	1	KSSKLVSANRLFG/SQEP
E9	1	KSSKSPSKKKKKKPGDC/SQEP
E10	2	KSSL/SQEP .
E11	1	KSSLEDQKIKEKLQPAEIETCMKTITTILEWLEKNQLAGKDEYEAKNKEAESVCAPIMSK IYQD/SQEP
E12	1	KSSLEEPDFYKTKIK/SQEP

=> d his

L2

L3

L4

(FILE 'HOME' ENTERED AT 06:58:21 ON 13 SEP 2000) SET COST OFF

FILE 'REGISTRY' ENTERED AT 06:58:25 ON 13 SEP 2000

E KSSKC/SQEP

E VIDHQGTKSSKCVRQKVEGSS/SQEP

1 S E3 L1

> FILE 'HCAOLD' ENTERED AT 06:59:13 ON 13 SEP 2000 0 S L1

FILE 'HCAPLUS' ENTERED AT 06:59:15 ON 13 SEP 2000 1 S L1

FILE 'REGISTRY' ENTERED AT 06:59:40 ON 13 SEP 2000

32 S E1-E32

14 S L4 AND PROTEIN/FS L5

SEL RN

18 S L4 NOT L5 L6

17 S L6 AND NUCLEIC/FS 1.7

Point of Contact: Jan Delaval Librarian-Physical Sciences CM1 1E01 Tel: 308-4498

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L8
              3 S L7 AND 747/SQL
L9
              4 S L7 AND 750/SQL
     FILE 'HCAOLD' ENTERED AT 07:01:28 ON 13 SEP 2000
              0 S L8 OR L9
L10
     FILE 'HCAPLUS' ENTERED AT 07:01:31 ON 13 SEP 2000
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L11
              1 S L3, L11
L12
L13
              O S LYS SER SER LYS CYS
L14
              1 S KSSKC
L15
              1 S L12, L14
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L16
L17
              0 S KSSKC
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L18
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FILE 'REGISTRY' ENTERED AT 07:04:18 ON 13 SEP 2000 E KSSKC/SQEP

=> d sqide can 11

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L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2000 ACS
RN 172998-82-2 REGISTRY
CN L-Serine, L-valyl-L-isoleucyl-L-alpha.-aspartyl-L-histidyl-L-
glutaminylglycyl-L-threonyl-L-lysyl-L-seryl-L-seryl-L-lysyl-L-cysteinyl-L-
valyl-L-arginyl-L-glutaminyl-L-lysyl-L-valyl-L-alpha.-glutamylglycyl-L-
seryl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 21
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SEQ 1 VIDHQGTKSS KCVRQKVEGS S

HITS AT: 1-21

MF C93 H161 N31 O33 S

SR CA

LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL

Absolute stereochemistry.

PAGE 1-B

PAGE 2-B

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

=> d sqide can 18 tot

ANSWER 1 OF 3 REGISTRY COPYRIGHT 2000 ACS L8

173012-28-7 REGISTRY RN

DNA (human-mouse clone 5G1.1 scFv DO12 immunoglobulin G1 anti-antigen CD CN 5-specifying) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

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     Deoxyribonucleic acid (human-mouse clone 5G1.1 scFv DO12 immunoglobulin G1
     anti-antigen CD 5-specifying)
FS
     NUCLEIC ACID SEQUENCE
SOL
     747
     159 a
             189 c
                             188 t
NA
                     211 g
NTE
     doublestranded
         1 atggccgata tccagatgac ccagtccccg tcctccctgt ccgcctctgt
SEQ
        51 gggcgatagg gtcaccatca cctgcggcgc cagcgaaaac atctatggcg
       101 cgctgaactg gtatcaacag aaacctggga aagctccgaa gcttctgatt
       151 tacggtgcga cgaacctggc agatggagtc ccttctcgct tctctggatc
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       501 cqqqcaqqqc ctqqaatqqa tqqqtqaqat cttaccqqqc tctqqtaqca
       551 ccgaatatgc ccaaaaattc cagggccgtg ttactatgac gcgtgacact
       601 tegaetagta cagtatacat ggagetetee ageetgegat eggaggacae
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CI
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SR
     CA
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               1 REFERENCES IN FILE CAPLUS (1967 TO DATE)
REFERENCE
            1: 124:127101
     ANSWER 2 OF 3 REGISTRY COPYRIGHT 2000 ACS
1.8
     173012-11-8 REGISTRY
RN
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CN
     5-specifying) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
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CN
     anti-antigen CD 5-specifying)
     NUCLEIC ACID SEQUENCE
FS
SQL
     747
NA
     161 a
             186 c
                     209 g
                             191 t
    doublestranded
NTE
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SEQ
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REFERENCE 1: 124:127101

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ANSWER 3 OF 3 REGISTRY COPYRIGHT 2000 ACS
L8
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     5-specifying cDNA) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
     Deoxyribonucleic acid (mouse clone 5G1.1M1 scFv immunoglobulin G1
ÇN
     anti-antigen CD 5-specifying messenger RNA-complementary)
FS
     NUCLEIC ACID SEQUENCE
SQL
     747
                             179 t
     183 a
             174 c
                     211 g
NA
     doublestranded
NTE
SEQ
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       151 tatggtgcaa ccaacttggc agatggcatg tcatcgaggt tcagtggcag
       201 tggatctggt agacagtatt atctcaagat cagtagcctg catcctgacg
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SR
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               1 REFERENCES IN FILE CAPLUS (1967 TO DATE)
            1: 124:127101
REFERENCE
=> d sqide can 19 tot
L9.
     ANSWER 1 OF 4 REGISTRY COPYRIGHT 2000 ACS
     173012-26-5 REGISTRY
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     5-specifying) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
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CN
     anti-antigen CD 5-specifying)
     NUCLEIC ACID SEQUENCE
FS
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SQL
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             223 c
                     198 g
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REFERENCE
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L9
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                             COPYRIGHT 2000 ACS
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     173012-18-5 REGISTRY
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CN
     5-specifying cDNA) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
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CN
     G1 anti-antigen CD 5-specifying messenger RNA-complementary)
     NUCLEIC ACID SEQUENCE
FS
SOL
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                             170 t
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                     197 g
NA
     163 a
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     5-specifying) (9CI) (CA INDEX NAME)
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CN
     anti-antigen CD 5-specifying)
FS
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REFERENCE
=> fil hcaplus uspatful
FILE 'HCAPLUS' ENTERED AT 07:04:53 ON 13 SEP 2000
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2000 AMERICAN CHEMICAL SOCIETY (ACS)
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=> d bib abs hitrn tot

FILE 'USPATFULL' ENTERED AT 07:04:53 ON 13 SEP 2000

CA INDEXING COPYRIGHT (C) 2000 AMERICAN CHEMICAL SOCIETY (ACS)

MF

CI

SR

LC

1.9

RN

CN

CN

FS

MF

CI

SR

LC

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L18
    ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2000 ACS
ΑN
     1996:73261 HCAPLUS
     124:127101
DN
TI
     Anti-complement C5 antibodies for the treatment of glomerulonephritis and
     other inflammatory diseases
     Evans, Mark J.; Matis, Louis; Mueller, Eileen Elliott; Nye, Steven H.;
IN
     Rollins, Scott; Rother, Russell P.; Springhorn, Jeremy P.; Squinto,
     Stephen P.; Thomas, Thomas C.; et al.
     Alexion Pharmaceuticals, Inc., USA
PA
     PCT Int. Appl., 159 pp.
SO
     CODEN: PIXXD2
DT
     Patent
     English
LΑ
FAN.CNT 1
     PATENT NO.
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                                          APPLICATION NO. DATE
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     _____
                     ____
                                          _____
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                     Al 19951109
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             SG, SI, SK, TJ, TM, TT, UA, UG, US, UZ, VN
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             SN, TD, TG
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                                         JP 1995-528523 19950501
PRAI US 1994-236208
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     WO 1995-US5688
                      19950501
     The use of anti-C5 antibodies, e.g., monoclonal antibodies, to treat
AB
     qlomerulonephritis (GN) is disclosed. The administration of such
     antibodies at low dosage levels has been found to significantly reduce
     glomerular inflammation/enlargement and other pathol. conditions assocd.
     with GN. Also disclosed are novel anti-C5 antibodies and anti-C5
     antibody-encoding nucleic acid mols. These antibodies are useful in the
     treatment of GN and other inflammatory conditions involving pathol.
     activation of the complement system.
TT
     172998-82-2P
     RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic
     use); BIOL (Biological study); PREP (Preparation); USES (Uses)
        (epitope KSSKC-contg. antigen; anti-complement C5 antibodies
        for the treatment of glomerulonephritis and other inflammatory
        diseases)
     173012-09-4P 173012-11-8P 173012-15-2P
IT
     173012-16-3P 173012-18-5P 173012-26-5P
     173012-28-7P
     RL: BAC (Biological activity or effector, except adverse); BOC (Biological
     occurrence); BPN (Biosynthetic preparation); PRP (Properties); THU
     (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP
     (Preparation); USES (Uses)
        (nucleic acid sequence; anti-complement C5 antibodies for the treatment
        of glomerulonephritis and other inflammatory diseases)
L18
    ANSWER 2 OF 2 USPATFULL
       2000:73908 USPATFULL
AN
       Use of antibodies specific to human complement component C5 for the
ΤI
       treatment of glomerulonephritis
IN
       Wang, Yi, Orange, CT, United States
       Matis, Louis, Southport, CT, United States
       Rollins, Scott, Monroe, CT, United States
       Alexion Pharmaceuticals, Inc., New Haven, CT, United States (U.S.
PΑ
```

corporation)

PI US 6074642 20000613

AI US 1994-236208 19940502 (8)

DT Utility

EXNAM Primary Examiner: Feisse, Lila; Assistant Examiner: Gambel, Phillip

LREP Fidel, Seth A.; Klee, Maurice M.

CLMN Number of Claims: 5 ECL Exemplary Claim: 1

DRWN 14 Drawing Figure(s); 7 Drawing Page(s)

LN.CNT 1197

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The use of anti-C5 antibodies, e.g., monoclonal antibodies, to treat glomerulonephritis (GN) is disclosed. The administration of such antibodies at low dosage levels has been found to significantly reduce glomerular inflammation/enlargement and other pathologic conditions associated with GN.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 172998-82-2P

(epitope KSSKC-contg. antigen; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)

IT 173012-09-4P 173012-11-8P 173012-15-2P 173012-16-3P 173012-18-5P 173012-26-5P 173012-28-7P

(nucleic acid sequence; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:22:05 2000; MasPar time 4.08 Seconds 57.866 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-487-283A-1 (8-12) from US08487283A.pep 35

1 KSSKC 5

Scoring table: PAM 150 Gap 15

142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 1000 summaries Maximum DB seq length 5

Database:

pir64 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 16.465; Variance 17.344; scale 0.949

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Score Match Length DB ID

Description

Pred. No.

No matches found.

Search completed: Wed Sep 6 08:23:04 2000 Job time: 59 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on:

Tabular output not generated. Wed Sep 6 08:19:32 2000; MasPar time 2.56 Seconds 60.533 Million cell updates/sec

Description: Perfect Score: Sequence: >US-08-487-283A-1 (8-12) from US08487283A.pep 35 1 KSSKC 5

Scoring table: PAM 150 Gap 15

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0% Listing first 1000 summaries Maximum DB seq length 5

Database:

swiss-prot38 1:swissprot

Statistics: Mean 16.989; Variance 16.059; scale 1.058

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID

Description

Pred. No.

No matches found.

Search completed: Wed Sep 6 08:20:17 2000 Job time: 45 secs.

SUMMARIES Result Query No. Score Match Length DB ID Description Pred. No.
. No. is the number of results predicted by ce greater than or equal to the score of the ris derived by analysis of the total score dis
Database: sptremb112 1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus Statistics: Mean 16.549; Variance 15.598; scale 1.061
Post-processing: Minimum Match 0% Listing first 1000 summaries Maximum DB seq length 5
Searched: 225878 seqs, 69334122 residues
Scoring table: PAM 150 Gap 15
Title: >US-08-487-283A-1 Description: (8-12) from US08487283A.pep Perfect Score: 35 Sequence: 1 KSSKC 5
ated. 60.308 Million co
Wed Sep 6 08:20:34 2000; MasPar time 5.75 Seconds
<u>~</u>

Search completed: Wed Sep $6\ 08:21:48\ 2000$ Job time : $74\ secs$.

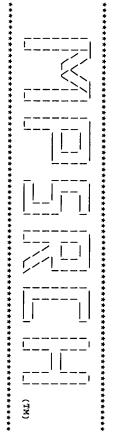
Search completed: Wed Sep 6 08:24:11 2000 Job time : 49 secs.	matches found.	SUMMARIES Result Query No. Score Match Length DB ID Description Pred. N	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.	Statistics: Mean 12.105; Variance 34.177; scale 0.354	Database: a-geneseq36 1:geneseqp	Post-processing: Minimum Match 0% Listing first 1000 summaries Maximum DB seq length 5	Searched: 188963 seqs, 23686106 residues	Scoring table: PAM 150 Gap 15	Title: >US-08-487-283A-1 Description: (8-12) from USO8487283A.pep Perfect Score: 35 Sequence: 1 KSSKC 5	Tabular output not generated.	time 2.62 Sec	e search, using Smith-Waterman	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993–1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	
		1								ares/sec	S 100	algorithm	3	(TM)

Search completed: Wed Sep 6 08:27:12 2000 Job time : 93 secs.	hes found.	Result Query No. Score Match Length DB ID Des	Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score d	Statistics: Mean 13.804; Variance 29.044;	Database: a-pending 1:PCT 2:U6 3:U60 4:U7 5:U80 6:U81 7: 10:U84B 11:U85 12:U86 13:U87 14:U88 18:U92 19:U93 20:U94 21:U95 22:NEWD 25:NEWU8 26:NEWU9	Post-processing: Minimum Match 0% Listing first 1000 summaries Maximum DB seg length 5	Searched: 820620 seqs, 123522873 residues	Scoring table: PAM 150 Gap 15	Title: >US-08-487-283A-1 Description: (8-12) from US08487283A.pep Perfect Score: 35 Sequence: 1 KSSKC 5	Tabular output not generated.	Run on: Wed Sep 6 08:25:39 2000; MasPar	<pre>MPsrch_pp protein - protein database search,</pre>	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993–1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	
		Description Pred. No.	cted by chance to have a of the result being printed, score distribution.	scale 0.475	6:U81 7:U82 8:U83 9:U84A 7 14:U88 15:U89 16:U90 17:U91 22:NEWP 23:NEWU60 24:NEWU7					no witition cert apages/sec	time 12.13 Se	using Smith-Waterman algorithm	lins, Biocomputing Research Unit. University of Edinburgh, U.K. hts by Oxford Molecular Ltd	(ML)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd srch_pp protein - protein database search, using Smith-Waterman algorithm n on: Wed Sep 6 08:24:29 2000: MasPar time 2.21 Seconds bular output not generated. tle: -US-08-487-283A-1 riccti Score: (8-12) from US09487283A.pep genece: 1 KSSKC 5 oring table: PAM 150 Gap 15 st-processing: Minimum Match 0% Listing first 100% Listing first 100% Maximum DB seq length 5 tabase: a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1 atistics: Mean 11.504; Variance 33.907; scale 0.339 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES SULT SCORE Match Length DB ID Description Pred. No.	Result Que	Pred. No. is t score greater and is derived	Statistics: M	essing:	Searched: 1	Scoring table: F	Title: > Description: (Perfect Score: 3 Sequence: 1	Run on: W	MPsrch_pp protein	Release 3 Copyright D	***************************************
· · · · · · · · · · · · · · · · · · ·	SUMMARIES ery tch Length DB ID Description Pred.	the number of results predicted by chance to have than or equal to the score of the result being by analysis of the total score distribution.	OMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 504; Variance 33.907; scale 0.3:	Minimum Match 0% Listing first 1000 Maximum DB seq len	15329240	PAM 150 Gap 15	487-; from 5	Wed Sep 6 08:24:29 2000; MasPar not generated. 34.699	- protein database search, using	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	

Search completed: Wed Sep $6\ 08:25:20\ 2000$ Job time : $51\ secs$.

No matches found.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:16:42 2000; MasPar time 4.45 Seconds 222.630 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-487-283A-1 (1-21) from US08487283A.pep 141 1 VIDHQGTKSSKCVRQKVEGSS 21

Scoring table: PAM 150 Gap 15

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

pir64 1:pirl 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 25.757; Variance 31.889; scale 0.808

SUMMARIES

22210987654321 32210987654321	Result No.
14 5 5 5 5 5 5 5 6 6 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	Score
100 0 48 9 48 6 46 1 44 7 44 7 42 6 43 3 41 1 41 1 41 1 41 1 41 1 41 1 41 1	Query Match
1676 936 936 213 213 214 1166 1002 1002 205 225 225 225 225 236 407 5407 553	Length 1
00000000000000000000000000000000000000	BB
CC5HU CC5MS H71862 B644567 T100479 T100879 T100879 T100879 A56678 A65068	甘
complement C5 precurs complement C5 precurs probable cytochrome C biogeness MADS box protein A hypothetical protein Anypothetical protein lactoferrin binding pyemanuclein-alpha - f hypothetical protein protein tyrosine phosprotein tyrosine phosprotein tyrosine phosprotein tyrosine phosprotein tyrosine phosprotein tyrosine phosprotein protein L34 N-carbamoylsarcosine globulin-1 - maize (f globulin-1 maize spore coat protein Sprotein	Description
2.35e-22 3.49e-03 3.07e-02 1.39e-01 2.29e-01 3.74e-01 6.08e-01 9.82e-01	Pred. No.

55 39.0 1349 2 T13931 nucleoporin - iruit five statements of the coat protein - 171391 spore coat protein (1 54 38.3 148 2 E47119 spore coat protein (1 54 38.3 224 1 G64383 riboflavin-specific d 54 38.3 249 2 T04337 M79 protein - rice statements of the coat protein statements of the coat protein - rice statements of the coat protein - rice statements of the coat protein statements o	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
.0 1349 2 F13931 nucleopox .0 1365 2 F13991 nucleopox .3 148 2 E47119 spore coa .3 224 1 G64383 riboflavi .3 224 2 T04337 M79 prote .3 249 2 T04335 MADS box .3 259 2 T04169 MADS box .3 259 2 T04169 MADS box .3 259 2 T04169 P element .3 818 1 A30107 dipeptidy .3 818 1 A30107 dipeptidy .3 818 2 T11742 egg sperm .3 1030 2 S57380 probable .6 116 1 Q4ADE2 early E4 .6 116 1 Q4ADE2 early E4 .6 116 2 G4ADE3 early E4 .6 116 2 S41772 glyciner6 231 2 T14801 MADS box .6 589 2 C38128 omega-cry .6 589 2 C38128 omega-cry .6 591 2 S43428 omega-cry .6 6918 2 D71407 hypotheti .6 1089 1 FFHUGA .6 1144 2 A54810 TMV resis .6 2471 2 A49128 cell-fate	53	53	53	53	53	53	53	53	53	53	53	54	54	54	54	54	54	54	54	54	55	ű
2 T13931 nucleopox 2 T13931 nucleopox 2 T13931 nucleopox 2 E47119 spore cox 2 T04333 riboflavi 2 T04335 MADS box 2 T04335 MADS box 2 T04169 Pelement 1 A30107 dipeptidy 2 T11742 egg sperm 2 S57380 probable 1 Q4ADE5 early E4 2 Q4ADE5 early E4 2 T14810 MADS box 2 T14810 epithelin 2 C38128 omega-cry 2 T14810 omega-cry 2 T14810 omega-cry 2 D71407 pypothetin 2 PFHUGA TMV resis 2 A49128 cell-fate	٠		٠	•	٠	•	•	•	•	•		•	٠	•		•			٠			٠
113931 nucleopor 113991 nucleopor 113991 spore co 1664383 riboflavi 104307 M79 prote 174335 MADS box 1704169 MADS box 1704169 MADS box 1704169 Pelement 130107 dipeptidy 1711742 egg sperm 171380 probable 04ADE5 early E4 941772 glycine r 174801 MADS box 174801 MADS box 174407 MADS box 174408 omega-cry 154205 galactosy 174407 platelet- 174810 TMV resis 174810 TMV resis 174810 TMV resis 174810 TMV resis	2471	1144	1089	918	669	591	589	231	148	116	116	1030	889	818	562	259	249	249	224	148	1365	1349
nucleopor nucleopor nucleopor spore cod riboflavi M79 prote MADS box MADS box P elament dipeptidy egg sperm probable early E4 early E4 glycine r MADS box MADS box F elament comega-cry galactosy hypotheti TMV resis cell-fate	N	N	H	N	N	N	N	N	N	,	м	N	Ν	ب	N	N	N	N	-	N	N	N
nucleoporin - iruit in nucleoporin - iruit in nucleoporin 154 - fru spore coat protein (i riboflavin-specific d M79 protein - rice MADS box protein - ri p element - fruit fly dipeptidyl aminopepti egg sperm receptor - probable membrane pro early E4 lik protein early E4 lik protein early E4 lik protein glycine-rich RNA-bind MADS box protein MADS box protein MADS epithelin/granulin promega-crystallin - gi galactosylceramidase hypothetical protein platelet-derived grow TMV resistance protei cell-fate determining	A49128	A54810	PFHUGA	D71407	I54205	S43428	C38128	T14801	S41772	Q4 ADES	Q4 ADE2	S57380	T11742	A30107	S46281	T04169	T04335	T04307	G64383	E47119	T13991	TEOST
	cell-fate determining	resis	platelet-derived grow	hypothetical protein	das	9	'n	MADS box protein MADS	rich	E4 11K	E4 11K	pable membrane	н	aminope	t - fruit	box protein - r		ס	riboflavin-specific d	coat	154 - fr	•

ALIGNMENTS

#cross-references #accession A01: ##molecule_typ ##residues A01: REFERENCE Lun A #journal J.]	REFERENCE #authors #journal #title	#title Molecular	##molecule ##residues ##cross-re ##note REFERENCE #authors	#authors #journal #title #cross-refere #accession	RESULT 1 ENTRY TITLE CONTAINS ORGANISM DATE ACCESSIONS REFERENCE
nces MUID:79005687 A01267 -type protein 678-751 ##label FER A01266 Lundwall, A.B.; Wetsel, R.A.; Kristensen, T.; Whitehead, A.S.; Woods, D.E.; Ogden, R.C.; Colten, H.R.; Tack, B.F. J. Biol. Chem. (1985) 260:2108-2112	PID:g179692 22, H.N.; Hugli, T.E. 23. Chem. (1978) 253:6955-6964 Structural analysis of the polypept C5a anaphylatoxin. Polypeptide sequ C5a graphylatoxin. Polypeptide seques an apply the coligosaccharide att	#title Molecular analysis of human complement component C5: localization of the structural gene to chromosome 9. #cross-references MUID:88209511 #accession A27689 ##molecule_type mRNA ##residues_ 412-1676 ##label WET ##cross-references GB:M65134; GB:M18879; NID:g179691; PIDN:AAA51856.1;	##molecule_type mRNA ##residues 1-1676 ##label HAV ##cross-references GB:M57729; NID:g179982; PIDN:AAA51925.1; PID:g179983 ##rothers	#authors Haviland, D.L.; Haviland, J.C.; Fleischer, D.T.; Hunt, A.; Wetsel, R.A. #journal J. Immunol. (1991) 146:362-368 #title Complete cDNA sequence of human complement pro-C5. Evidence of truncated transcripts derived from a single copy gene. #cross-references MUID:91079575 #acrossion A40075	on_name man 30-Sep-1992 #text_changons15121

US-08-487-283A-1.rpr

```
##Cross-references GDB:119734; OMIM:120900
#map_position 9q34.1-9q34.1
CLASSIFICATION #superfamily alpha-2-macroglobulin
KEYWORDS complement alternate pathway; cytolysis;
glycoprotein; inflammation; membrane attack complex; plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #product C5b alpha' chain #status predicted #label C5BA\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
  Isolation and sequence analysis of a cDNA clone encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complement C5 contains two disulfide-linked chains, formed by removal of four basic residues. C5 convertuse releases C5a anaphylatoxin from the amino end of the alpha chain, generating C5b (beta and alpha" chains).
Activation of C5 initiates the spontaneous assembly of the late complement components, C5-C9, into the membrane attack complex. C5b has a transient binding site for C6. The C5b-C6 complex is the foundation upon which the membrane attack complex is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #label C5A\
#product C5a anaphylatoxin #status experimental #label
C5T\
                                                                                                                                                                                                                                                                                                                                                                                                                       #title Group B streptococci inactivate complement component C5a by enzymic cleavage at the C-terminus. #cross-references MUID:91144547
                                                                                                                                                                                                                                                                                                                 S15121
Subsect, J.F.; Mollison, K.W.; Buko, A.M.; Ashworth, J.C.; Hill, H.R.
Biochem. J. (1991) 273:635-640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #domain signal sequence #status predicted #label SIG\
#product complement C5 #status predicted #label MAT\
#product C5D #status predicted #label C5B\
#product complement C5 and C5b beta chain #status
predicted #label C5BB\
#product complement C5 alpha chain #status
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#binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #cleavage_site Arg-Leu (C5 convertase) #status
experimental\
#binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                            'SLALSPRIECNGKISGHCKLRLPGSSDSPASASQVAGITGTHHHAQPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                       the carboxyl-terminal part of the sequence in this report appears to be derived from translation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #molecular-weight 188330 #checksum 3858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C5a has potent spasmogenic and chemotactic activity,
                           fifth complement component.
#cross-references MUID:85130937
#accession A01266
                                                                                                                                                                                                                                                                                              ALU repeat sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   experimental/
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##cross-references GB:K02874
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#length 1676 #m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            annotation
                                                                                             ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             assembled
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698-724,699-731,
711-732,866-1527,
1101-1159,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-673,678-1676
19-673,752-1676
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                                                                                                                                 ##residues
                                                                               #accession
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1405-1474,
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1532-1606,
1553-1676,
1654-1657
                                                                                                                                                                                                                                    ##note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #contents
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                                                                                                                                                                                                                                                                                                                                               #authors
                                                                                                                                                                                                                                                                                                                                                                                                   #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     678-751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            751-752
#title
                                                                                                                                                                                                                                                                                                                    REFERENCE
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#authors Haviland, D.L.; Haviland, J.C.; Fleischer, D.T.; Wetsel, R.A. #journal J. Blol. Chem. (1991) 266:11818-11825
#title Structure of the murine fifth complement component (C5) gene. A large, highly interrupted gene with a variant donor splice site and organizational homology with the third and fourth complement component genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement alternate pathway; complement pathway; cytolysis; glycoprotein; inflammation; membrane attack complex; plasma
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#product C5b alpha' chain #status predicted #label C5BA\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #introns 22/3; 86/3; 140/3; 164/3; 195/2; 223/1; 253/2; 291/3; 334/1; #introns 22/3; 86/3; 140/3; 164/3; 195/2; 223/1; 253/2; 291/3; 334/1; 312/3; 434/3; 502/3; 612/3; 61/1; 691/1; 757/1; 787/2; 812/1; 818/4; 935/1; 985/1; 1056/1; 1081/2; 1134/3; 1166/3; 1224/1; 1292/3; 1343/3; 1364/3; 1392/1; 1445/3; 1445/3; 1506/1; 1534/1; 1564/1; 1592/1;
                                                                                                                                                                                                                                                   #authors Wetsel, R.A.; Fleischer, D.T.; Haviland, D.L.
#journal J. Biol. Chem. (1990) 265:2435-2440
#title Deficiency of the murine fifth complement component (C5). A
2-base pair gene deletion in a 5'-exon.
#cross-references MUID:90153853
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TO Complement C5 contains two disulfide-linked chains, formed by removal of four basic residues. C5 convertase releases C5a anaphylatoxin from the amino end of the alpha chain, generating C5b (beta and alpha' chains).

TACIVATION Of C5 initiates the spontaneous assembly of the late complement components, C5-C9, into the membrane attack complex. C5b has a transient binding site for C6. The C5b-C6 complex is the foundation upon which the membrane attack complex is
                                                                                                                                                                                                                                                                                                                                                                                                               ##nolecule_type mRNA
##residues_type mRNA
##residues_teferences GB:W35526; GB:U05234; NID:g192302; PIDN:AAA37348.1;
##cross-references PID:g309123
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                                                                                                            #formal_name Mus musculus #common_name house mouse
19.Nov-1988 #sequence_revision 15-Oct-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primary structure of the fifth component of murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assembled.
C5a has potent spasmogenic and chemotactic activity.
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Biochemistry (1987) 26:737-743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type mRNA ##residues 'PGL',44-1680 ##label WET2
                             C5MS #type complete complement C5 precursor - mouse
                                                                                                                                                                    18-Jun-1999
A35530, A27538; A40429
A35530
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cession A40429
##molecule_type DNA
1-15 ##label HAV
                                                                                     C5a anaphylatoxin; C5b
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19-674,756-1679
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Best Local
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Best Local Similarity 47.1%;
Matches 8; Conservative
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#title
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1524-1529,
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702-728,703-735,
715-736,870-1531,
                    #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #title Genomic sequence comparison of two unrelated isolates of human gastric pathogen Helicobacter pylori.
#cross-references MUID:99120557
#accession H71862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors
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                                                                                                                                                                                                                                                                                                                                                                                                    ##residues 1-936 ##label ARN
##cross-references GB:AE001528; GI
##experimental_source strain J99
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##molecule_type DNA
##rocid...-
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Similarity 50.0%;
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Nature (1999) 397:176-180
                                                                                  #formal_name Helicobacter pylori
09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
                                                                                                                      cytochrome
26695)
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#length 936 #molecular-weight 106452 #checksum
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12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
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pmb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
                                                                    10-Oct-1997
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#binding_site carbohydrate (Asn) (covalent) #status
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c biogenesis protein - Helicobacter pylori (strain
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Pred. No. 3.83e-03;
7; Mismatches 2;
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H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujil, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, W.S.; Venter, J.C.
#journal Nature (1997) 388:539-547
#title Helicobacter pylori.
#cross-references MUID:97394467
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ENTRY
TITLE
ORGANISM
                                                                                                        RESULT
ENTRY
                                                                                                                                                                                                                                                                                                                                                                ##cross-references EMBL:025696; NID:g1199574; PID:g1049022
##experimental_source tissue_type inflorescence meristems
CLASSIFICATION #superfamily transcription factor squa; serum re
DNA-binding domain homology
KEYWORDS DNA binding; transcription regulation
SUMMARY #length 213 #molecular-weight 24408 #checksum
                                                                ORGANISM
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Best Local
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#journal plant J. (1996) 9:399-408
#title Identification of two MADS box genes that are expressed in the apical meristem of the long-day plant Sinapis alba in transition to flowering.
#cross-references MUD:97077349
                                          #variety
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
##residues 1-213 ##label MEN
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TIGR:HP0378
Y #length 936 #molecular-weight 106359 #checksum 8931
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                                                                                                                                                                                                                                                                                                  y Match 44.7%;
Local Similarity 53.3%;
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Local Similarity 55.0%; Pred. No.
hes 11; Conservative 3; Misma
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MADS box protein A - white mustard
#formal_name Sinapis alba #common_name white mustard
16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
                                                            $76070 #type complete hypothetical protein - Syne #formal_name Synechocystis
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                      25-Apr-1997 #sequence_revision
                                                                                                                                                                                                                                                                                    Conservative
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21-Aug-1998
                                              6803
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                                                                                                                                                                                                                                                                                                    Score 63; DB 2; L
Pred. No. 8.46e-02;
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. No. 3.07e-02;
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                      25-Apr-1997 #text_change
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#superfamily transcription factor squa; serum response factor DNA-binding domain homology
DNA binding; nucleus; transcription regulation
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##cross-references EMBL:D63999; GB:AB001339; NID:g1001396; PID:d1010699;
##ross-references EMBL:D63999; GB:AB001339; NID:g1001396; PID:d1010699;
##note the nucleotide sequence was submitted to the EMBL Data
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                     #authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Matuo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S. Yasuda, M.; Tabata, S. Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S. Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S. Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S. Tayanabactari, Solon Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

#accession S76070
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Arabidopsis thaliana chromosome II BAC F17K2 genomic
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homology #label SRF
#length 214 #molecular-weight 24533 #checksum 6965
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#length 213 #molecular-weight 22745 #checksum 2191
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Pred. No. 2.29e-01;
4; Mismatches 4; Indels
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Best Local Similarity 46.7%;
Matches 7; Conservative
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Best Local Similarity 35.0%;
Matches 7; Conservative
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##INOLALE_LYPE JAN
##residues
1-940 ##label PET
##residues
1-940 ##Label PET
##cross-references EMBL:X79838; NID:g509053; PID:g509054
##cross-references EMBL:X79838; NID:g509053; PID:g509054
##cross-references EMBL:X79838; NID:g509053; PID:g509054
##cross-references EMBL:X79838; NID:g509053; PICATION #superfamily tonB-dependent receptor carboxyl-terminal homology
H71609 #type complete
hypothetical protein PFB0630c - malaria parasite (Plasmodium
                                                                                                                                                                                                                                          Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, B.V.; Shallom, S.; Mason, T.; Yu, K.; Fujii, C.; Pederson, J.; Shen, K.; Jing, J.; Aston, C.; Lai, Z.; Schwartz, D.C.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Fraser, C.M.; Adams, M.D.; Venter, J.C.; Hoffman, S.L. Science (1998) 282:1126-1132
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Poolman, X.Y.Z.; Tommassen, X.Y.Z.
submitted to the EMBL Data Library, June 1994
Molécular charactarization of the structural gene for the
lacto-ferrin receptor of the meningococcal strain H44/76.
849087
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lactoferrin binding protein - Neisseria meningitidis
#formal_name Neisseria meningitidis
16-Feb-1995 #sequence_revision 12-May-1995 #text_change
10-Jul-1998
                                                                                       #formal_name Plasmodium falciparum
13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   #title Chromosome 2 sequence of the human malaria parasite
Plasmodium falciparum.
#cross-references MUID:99021743
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Pred. No. 3.74e-01;
3; Mismatches 6; Indels
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Pred. No. 6.08e-01;
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50.0%;
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Best Local Similarity 43.8%;
Matches 7; Conservative
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Best Local Similarity 50.0%;
Matches 6; Conservative
                                  Matches
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Best Local Similarity
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#journal Mech. Dev. (1992) 37:69-80
#title The yemanuclein-alpha: a new Drosophila
specific for the oocyte nucleus.
#cross-references_MUID:92297435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #introns
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                                                                                                                                                                                                                                      #accession
                                                                                                                                                                                                                                                    #title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
                                                                                              ##molecule_type DNA
##residues 1-164 ##label BLAT
##cross-references GB:AB000368; GB:U00096; NID:g2367165; PID:g2367166;
##cross-references GB:AB000368; GB:U00096; NID:g2367165; PID:g2367166;
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##cross-references FlyBase:FBgn0005596
trons 80/3; 154/3; 428/1 477/2; 557/2
RDS DNA binding; oocyte
RY #length 1002 #molecular-weight
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QQGNRESKSIRRNIE 92
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                               41.1%;
larity 40.0%;
Conservative
                                                                                                                                                                                                                                      A65068
                                                                                                                                                                                                                                                                                     Science (1997) 277:1453-1462
                                                                                                                                                                                                                                                                                                                                                                                                                                    A65068 #type complete
hypothetical protein b2848 - Escherichia coli (strain K-12)
#formal_name Escherichia coli
12-Sep-1997_#sequence_revision 17-Sep-1997 #text_change
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yemanuclein-alpha - fruit fly (Drosophila melanogaster)
#formal_name Drosophila melanogaster
08_Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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A56678; S22146
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                               Score 58; DB 2; I
Pred. No. 9.82e-01;
6; Mismatches
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Pred. No. 6.08e-01;
5; Mismatches 1
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Best Local Similarity 25.0%; Pred. No. 9.82e-01;
Matches 5; Conservative 9; Mismatches (
                                                                                                Query Match
Best Local
                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                   #authors Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E. #journal J. Biol. Chem. (1995) 270:26782-26785 #title A single mutation converts a novel-phosphotyrosine binding domain into a dual-specificity phosphatase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-205 ##label RES
##cross-references EMBL:U34973; NID:g1063624; PID:g1063625
FICATION #superfamily VH1-type dual specificity phosphoprotein
phosphatase homology
                                                                                                                                                                                                                                                                                                                  ##molecule_type mRNA
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                                              51 ILQKHGITHIICIRQNIEAN 70
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                 VIDHQGTKSSKCVRQKVEGS
                                                                                                  Similarity
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protein tyrosine phosphatase - mouse
formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                                                                                                                                                                                *superfamily VH1-type dual specificity phosphoprotein phosphatase homology
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#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
17-Mar-1999
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phosphatase homology #label VH1
                                                                                                                                                                                                                                                                                                                                  preliminary; translated
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    phosphatase homology #label VH1
pth 205 #molecular-weight 23683 #checksum 2745
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1 223 #molec
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25.0%;
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                                                                                                                                                #molecular-weight 25416
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Pred. No.
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                                                                                                DB 2; I
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##residues
1-259 ##label COL
##cross-references GB:282098; GB:AL123456; NID:g3261664; PID:e280727;
##cross-references PID:g1666111
 F70677 #type complete
hypothetical protein Rv3549c - Mycobacterium tuberculosis
(strain H37RV)
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ribosomal protein L34 - human
#formal_name Homo sapiens #common_name man
24-May-1996 #sequence_revision 24-May-1996 #text_change
13.Aug-1999
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#superfamily ribitol dehydrogenase; short-chain alcohol
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#title Generation of a transcription map at the HSD17B locus
#cross-references WUID:96039267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rommens, J.M.; Durocher, F.; McArthur, J.; Tonin, P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references GB:L38941; NID:g1008855; PIDN:AAC41916.1;
PID:g1008856
PID:g1008856
FICATION #superfamily rad ribosomal protein L34
#length l17 #molecular-weight 13305 #checksum 4392
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#length 259 #molecular-weight 26855 #checksum 5885
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##molecule_type mRNA
##residues 1-117 ##label RES
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14
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Query Match 40.4%; Score 57; DB 2; Length 117;
Best Local Similarity 41.7%; Pred. No. 1.58e+00;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Db 80 GSMCAKCVRDRI 91
|::||||::|
Qy 6 GTKSSKCVRQKV 17
Search completed: Wed Sep 6 08:17:01 2000
Job time: 19 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:15:20 2000; MasPar time 2.98 Seconds 218.703 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-08-487-283A-1 (1-21) from US08487283A.pep 141 1 VIDHQGTKSSKCVRQKVEGSS 21

Sequence:

Scoring table: PAM 150 Gap 15

85661 seqs, 30989116 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 26.489; Variance 29.186; scale 0.908

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2221184 23210987654 23210987654	Result No.
14 00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Score
100 0 48.6 0 42.6 0 41.8 4 41.1 8 41.1 8 40.4 4.1 1 39.7 7 39.7 7 39.7 7 39.7 7 39.7 7 37.6 6	Query Match
1676 4280 943 1002 160 116 116 264 87 573 1357 775 775 148 818 818 819 1039 1039 1039 1039 1039 1039	Length I
	BB
COS_HUMAN COS_MOUSE IM44_CABEL IROA_NEIME YEMA_DROME YEMA_DROME YOU_ECOLI RL34_HUMAN CSH_ARTS IT16_ARTS IT16_ARTS PSEPD YENA_YENA COTZ_BACSU QAPZ_YEAST HS97_STRPU YER71_CAEEL YER71_CAEEL E411_ADE02 E411_ADE02 E411_ADE03 GRN_MOUSE GALC_HUMAN GALC_MACMU	ID
COMPLEMENT C5 PRECURSO COMPLEMENT C5 PRECURSO PROBABLE MITOCHONDRIAL IRON-REGULATED OUTER MYEMANUCLEIN-ALPHA. HYPOTHETICAL 18.7 KDA 60S RIBOSOMAL PROTEIN NO-CARBAMOYLSARCOSINE A PUTATIVE TRYPSIN INHIBSPORE COAT PROTEIN SPOTEIN-1 S ALLELE PR DNA-DIRECTED RNA POLYM TRANSPOSON TX1 HYPOTHE SPORE COAT PROTEIN Z. PUTATIVE 5-AMINO-6-(5-DIREPTIDYL AMINOPEPTID SPOTE COAT PROTEIN Z. PUTATIVE 5-AMINO-6-(5-DIREPTIDYL AMINOPEPTID PROBABLE EARLY E4 11 K PROBABLE EARLY E4 11 K PROBABLE EARLY E4 11 K GRAUNLINS PRECURSOR (A GALACTOCEREBROSIDASE P GALACTOCEREBROSIDASE P	Description
3.33e-25 7.23e-04 1.11e-01 1.88e-01 3.19e-01 3.19e-01 5.36e-01 5.36e-01 8.95e-01 8.95e-01 8.95e-01 1.44e+00 2.44e+00 2.44e+00 2.44e+00 2.44e+00 2.44e+00 2.44e+00 2.44e+00 3.44e+	Pred. No.

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36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.9	36.9	36.9	36.5	36.9	36.5	36.9	37.6
1651 1678	1132	1129	1056	588	574	512	470	470	337	337	121	121	1620	455	354	329	185	121	64	1089
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VIT6_CAEEL	JAK2_RAT	JAK2_MOUSE	MUC5_HUMAN	GRN_RAT	ESR1_ONCMY	VP67_NPVAC	KPY1_SALTY	KPY1_ECOLI	VP67_NPVGM	ADH1_ZYMMO	R34B_YEAST	R34A_YEAST	MIDM_MOUSE	P2X5_RAT	OCD_AGRTS	ESG2_TRYBB	EFP_BACFR	RK14_GUITH	BFD_SERMA	PGDS_HUMAN
CLATHRIN HEAVY CHAIN.	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TRACHEOBRONCHIAL MUCIN	GRANULINS PRECURSOR (A	ESTROGEN RECEPTOR (ER)	Ę	PYRUVATE KINASE I (EC	PYRUVATE KINASE I (EC	MAJOR ENVELOPE GLYCOPR	ALCOHOL DEHYDROGENASE	60S RIBOSOMAL PROTEIN	60S RIBOSOMAL PROTEIN	(CYTOSINE-5)-ME	P2X PURINOCEPTOR 5 (AT	ORNITHINE CYCLODEAMINA	VSG EXPRESSION SITE-AS	ELONGATION FACTOR P (E	CHLOROPLAST 50S RIBOSO	BACTERIOFERRITIN-ASSOC	ALPHA PLATELET-DERIVED
1.04e+01 1.04e+01	1.04e+01	1.04e+01	1.04e+01	1.04e+01	1.04e+01	1.04e+01	1.04e+01	1.04e+01	1.04e+01	1.04e+01	1.04e+01	1.04e+01	6.49e+00	6.49e+00	6.49e+00	6.49e+00	6.49e+00	6.49e+00	6.49e+00	4.00e+00

ALIGNMENTS

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A MEDULINE; 9/32508.

Thang X. Boyar W., Toth M.J., Wennogle L., Gonnella N.C.;

"Structural definition of the C5a C terminus by two-dimensional nuclear magnetic resonance spectroscopy.";

Proteins 28:261-267(1997).

Proteins 28:261-267(1997).

Proteins 28:261-267(1997).

The proteins 28:261-267(1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SIMILÂRITY: TO C3, C4 AND ALPHA-2-MACROGLOBULIN.
-:- SIMILARITY: CONTAINS 1 ANAPHYLAFORIN-LIKE DOMAIN.
-:- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 855
ONWARD DUE TO THE PRESENCE OF AN ALU REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                               Zuiderweg E.R., Fesik S.W.;
"Heteronuclear three-dimensional NMR spectroscopy of the inflammatory
                                                                                                           Zuiderweg E.R., Mollison K.W., Henkin J., Carter G.W.;
Sequence-specific assignments in the 1H NMR spectrum of the human
inflammatory protein Cfa ".
                                                                                                                                                                                                                                                                Zuiderweg E.R., Nettesheim D.G., Mollison K.W., Carter G.W.; "Tertiary structure of human complement component C5a in solution from nuclear magnetic resonance data."; Biochemistry 28:172-185(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang X., Boyar W., Galakatos N., Gonnella N.C.; "Solution structure of a unique C5a semi-synthetic antagonist: implications in receptor binding."; Protein Sci. 6:65-72(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Siochemistry 28:2387-2391(1989).
                                                                                                                                                          inflammatory protein C5a.";
Biochemistry 27:3568-3580(1988).
cleavage at the C-terminus.";
Biochem. J. 273:635-640(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR OF C5A.
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1CFA; 17-SEP-97,
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                                                                                      MEDLINE; 88309754.
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                                                                   STRUCTURE BY NMR
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Wetsel R.A., Ogata R.T., Tack B.F.;
Biochemistry 26:737-743(1987).
-!- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS, C5-C9, INTO THE MEMBRANC ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYTIC COMPLEX IS ASSEMBLED.
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"Deficiency of the murine fifth complement component (C5). A 2-base
pair gene deletion in a 5'-exon.";
                                                                                                                                                   Complement pathway; Complement alternate pathway; Glycoprotein; Plasma; Membrane attack complex; Cytolysis; Inflammatory response; Signal; Polymorphism; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C
CS ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS.
INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCRASES VASCULAR
PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 3.33e-25;
0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                               COMPLEMENT C5 ALPHA CHAIN
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01-NOV-1990 (Rel. 16, Last sequence update)
01-EEB-1986 (Rel. 33, Last annotation update)
COMPLEMENT C5 PRECURSOR [CONTAINS: C5A ANAPHYLATOXIN].
                                                                                                                                                                                                                           COMPLEMENT C5 BETA CHAIN
PFAM; PF00207; A2M; 1.
PFAM; PF01835; A2M_N; 1.
PFAM; PF01831; ANATO; 1.
PFAM; PF0179; NTR; 1.
PRINTS; PR00004; ANAPHYLATOXN.
PROSITE; PS0177; ANAPHYLATOXN.
PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
PROSITE; PS01179; ANAPHYLATOXIN_1; 1.
                                                                                                                                                                                                                                                                                                 C5B (ALPHA').
ANAPHYLATOXIN-LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1676 AA; 188331 MW;
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SEQUENCE OF 41-1680 FROM N.A.
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Local Similarity 100.0%;
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HSSP; P01031; ....

MGD; MGI:96031; HC.

PFAM; PF00207; A2M; 1.

PFAM; PF01835; A2M_N; 1.

R PFAM; PF01835; A2M_N; 1.

R PFAM; PF01821; ANATO; 1.

R PFAM; PF01759; NTR; 1.

PR PRINTS; PR00004; ANAPHYLATOXN.

DR PROSITE; PS00177; ANAPHYLATOXN_1; 1.

DR PROSITE; PS01177; ANAPHYLATOXIN_2; 1.

Complement pathway; Complement alternate pathway; Glycoprotein;

Complement pathway; Complex; Cytolysis; Inflammatory response;
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or send a
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  Caenorhabditis elegans
                                                                PROBABLE MITOCHONDRIAL
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SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOYAL OF 4 RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULBOND. C5 CONVERTASE ACTIVATES C5 BY CLEAVING THE ALPHA CHAIN, RELEASING C5A ANAPHYLATOXIN & GENERATING C5B (BETA CHAIN + AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY:
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A35530; A35530.
; P01031; 1KJS.
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                                                            (Rel. 38, Created)
(Rel. 38, Last sequence update)
(Rel. 38, Last annotation update)
rOCHONDRIAL IMPORT INNER MEMBRANE
                                                                                                                                                                     STANDARD;
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MISSING (IN DEFECTIVE VARIANT C5D)
W; 81EB5A16FAC7D95C CRC64;
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Y -> L (II
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                                                              SUBUNIT TIM44
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                                                                                                                                                                                                                                                                             Q06379;
01-NOV-1995 (Rel. 32,
01-NOV-1995 (Rel. 32,
01-FEB-1996 (Rel. 33,
                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                  STRAIN-BNVC
                                                                                                                                                                                                                                             Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion; Inner membrane; Transport; Protein Translocation; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U97405; AAB53011.1; -.
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                                                                                                                                                             Pettersson A., van der Ley P., Poolman J.T., Tom
Molecular characterization of the 98-kilodalton
                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                     IRON-REGULATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WORMPEP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute. There by non-profit institutions as long as ified and this statement is not removed.
                                                                                          SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS
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sen the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                  subdivision; Neisseriaceae; Neisseria.
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lon update)
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             http://www.isb-sib
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ton iron-regulated
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7 TKSSKCVRQKVE 18
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P49207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEDLINE: 92297435.
MEDLINE: 92297435.
Ait-Ahmed O., Bellon B., Capri M., Joblet C., Thomas-Delaage M.;
Ait-Ahmed I., Bellon B., Capri M., Joblet C., Thomas-Delaage M.;
The yemanuclein alpha: a new Drosophila DNA binding protein specific
                      PFAM; PF00593; TOTB_DOXC; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X65502, 22.46.
PIR; S22146; S22146.
FLYBASE; FEGRO005596; yem-alpha.
Nuclear protein; DNA-binding; Repeat.
DOMAIN 80 85 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                         IRON-REGULATED OUTER MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mech. Dev. 37:69-80(1992).

-!- FUNCTION: MAY PLAY A KEY ROLE IN EGG ORGANIZATION. IT MAY BE TRANSCRIPTIONAL REGULATOR.

-!- SUBCELLULAR LOCATION. UNCLEAR.

-!- TISSUE SPECIFICITY: OOCYTE-SPECIFIC.

-!- PTW: THE N-TERNINGS IS BLOCKED.
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Pred. No. 1.88e-01;
5; Mismatches 1; Indels
                                                                                                                                            Score 59; DB 1; Length 943; Pred. No. 1.88e-01; 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> L (IN CDNA SEQUENCE).
EE69A384EBA24D2F CRC64;
                                                                                        28 943 IRON-REGULATED OUTER MEMBRA
826 943 TONB C-TERMINAL BOX.
943 AA; 105424 WW; 5AC578F5CB4D8641 CRC64;
                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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Best Local Similarity 50.0%;
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           EMBL; X69214; CAA49148.1;
                                                                                                                                                                                                                                                                                 STANDARD;
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1002 AA;
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Best Local Similarity
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826
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P25992;
                                                                                                       SIMILAR
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                            Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davis K.,
Kurdi O.,
                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis Duncon M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
YQEJ_ECOLI STANDARD; PRT; 160 AA.
Q46643; P77135;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 18.7 KDA PROTEIN IN KDUI-LYSS INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 160;
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160 AA; 18719 MW; 10910D39F2B5F70D CRC64;
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Pred. No. 3.19e-01;
6; Mismatches 3;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-2000 (Rel. 39, Last annotation update)
60S RIBOSOMAL PROTEIN L34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 AA
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EMBL, AE000038; AAC75887.1; ALT_INIT.
EMBL, U83187; AAB40287.1; - ECGENE; EG13101; yqeJ.
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TRANSMEM 8
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 97426617.
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MEDLINE; 96039267
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RESULTATION OF THE PROPERTY OF
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or send a
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                                                                                                                                            "Crystallographic and fluorescence studies of carbamoylsarcosine amidohydrolase from Arthro J. Mol. Biol. 263:269-283(1995)
-I- CATALYTIC ACTIVITY: N-CARBAMOYLSARCOSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
N-CARBAMOYLSARCOSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P32400;
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kenmochi N., Kawaguchi T., Rozen S.,
Hudson T.J., Tanaka T., Page D.C.;
"A map of 75 human ribosomal protein
Genome Res. 8:509-523(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rommens J. Allen T.,
                                          -!- COFACTOR: ONE SULFATE ION PER SUBUNIT

!- PATHWAY: DECRADATION OF CREATININE TO

-!- SUBUNIT: HOMOTETRAMER.

PIR: 528969; $28969.
                                                                                                                                                                                                                              MEDLINE; 97070380.
Zajc A., Romao M.J
                                                                                                                                                                                                                                                                                                                                 sp.
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 92;
Romao M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribosomal protein.
INIT_MET 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L38941; AAC41916.1; -.
EMBL; AB007181; BAA25840.1; -.
PFAM; PF01199; R1bosomal_L34e; 1.
PROSITE; PS01145; RIBOSOMAL_L34E;
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lon update)
19 PRECURSOR.
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                                                                                                                                                        update)
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5.36e-01;
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; eurosids II;
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Adams M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borodin A. M., Danilkovich A.V., Chernov I.P., Azhykina T.L.,
Rostapshov V.M., Monastyrskaya G.S.;
Rostapshov V.M., Monastyrskaya G.S.;
"Genes coding for RNA polymerase in bacteria. III. The use of
modified Sanger's method for sequencing the C-terminal region of rpoB
gene, N-terminal region of rpoC gene and intercistron region of RNA
polymerase in Pseudomonas putida.";
ploorg. Khim. 14:1179-1182(1988).

-:- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                             PROTEINS, RESPECTIVELY.
SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCININ, ETC.).
                                                                                              Biochem. Genet. 27:239-251(1989).
-!- PTW: THREF PROCESSING STEPS OCCUR IN THE FORMATION OF THE MATURE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT.
-!- POLYMORPHISM: THE THRE MOST COMMONLY OCCURRING GLB1 ALLELES HAVE THE DESIGNATION L. I. AND S FOR LARGE, INTERMEDIATE, AND SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borodin A.M., Danilkovich A.V., Allikmets R.L., Rostapshov V.M., Chernov I.P., Azhikha T.L., Monastyrskaya S., Sverdlov D.; "Nucleotide sequence of the ryob gene coding for the beta-subunit of RNA polymerase in Pseudomonas putida."; Dokl. Blochem. 302:1261-1265(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6) (TRANSCRIPTASE
BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas putida.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                            "Characterization of embryo globulins encoded by the maize Glb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB 1; Length 573; Pred. No. 8.95e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525ED1D00A062976 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLOBULIN-1 S ALLELE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR 21 (POTENTIAL).
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58.3%;
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SEQUENCE OF 87-100.
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                      89374022
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P19175;
                        MEDLINE;
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Belanger F.C., Kriz A.L.;
"Molecular characterization of the major maize embryo globulin encoded by the Glb1 gene.";
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Magnoliophyta; Liliopsida; Poales; Poaceae; 2ea.
SEQUENCE FROM N.A.
MEDLINE; 90097939.
Fosnaugh K.L., Loomis W.F.;
"Spore coat genes SP60 and SP70 of Dictyostelium discoideum.";
MOI. Cell. Biol. 9:5215-5218(1989).
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SIGNAL
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Pred. No. 8.95e-01;
4; Mismatches 1; Indels
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5.5 X 11 AA TANDEM REPEATS.
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0EA20BDC96DE2A19 CRC64;
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01-ADG-1990 (Rel. 15, Last sequence update)
15-UZL-1999 (Rel. 38, Last annotation update)
GLOBULIN-1 S ALLELE PRECURSOR (GLB1-S) (7S-LIKE).
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PRESPORE MOTIF 1.
PRESPORE MOTIF 2.
PRESPORE MOTIF 3.
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                                                                                                                   PRELIMINARY SEQUENCE OF 72-170 FROM N.A.
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ilarity 54.5%;
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PIR; B25439; B25439.
DICTYDB; DD03009; COTB.
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8 KSSKCVRQKVE 18
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Best Local Similarity
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01-JAN-1990 (
01-JAN-1990 (
01-APR-1990 (
                                                                                                                             PIR; A32494; A32494; A32494, PRINTS; PRO0939; C2HCZNFINGER.
Hypothetical protein; Transposable element.
SEQUENCE 775 AA; 82355 MW; B8C361AEC65DD85B CRC64;
                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Last annotation update)
TRANSPOSON TX1 HYPOTHETICAL 82 DA PROTEIN (ORF 1).
Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphiba; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Garrett J.E., Knutzon D.S., Carroll "Composite transposable elements in Mol. Cell. Biol. 9:3018-3027(1989).
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PROSITE; PS01166; RNA_POL_BETA;
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CONFLICT 1:
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SUBUNIT: THE
ENZYME WHICH
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CATALYTIC ACTIVITY: N
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een the Swiss Institute of Bioinformatics and the EN
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SNTSKCVSSEVEGTP
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                                          h 39.0% Similarity 46.7% 7; Conservative
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Best Local :
Matches
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Q58085;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-FEB-2000 (Rel. 39, Last annotation update)
PUTATIVE 5-AMINO-6-(5-PHOSPHORIBOSYLAMINO)URACIL
(EC_1.1.1.193) (HTP REDUCTASE).
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15-FEB-2000
SPORE COAT P
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J. Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I. Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is published the Swiss Institute of Bioinformatic the European Bioinformatics Institute. These use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 1
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EMBL; Z99110; CAB13031.1;
PIR; E47119; E47119.
SUBTILIST; BG10499; COTZ.
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Bacillus subtilis;";
J. Bacteriol. 175:3757-3766(1993).
-i- SUBUNIT: DISULFIDE CROSS-LINKED
-i- SUBCELLULAR LOCATION: SPORE OUTE
-i- SIMILARITY: TO COTY.
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                                                                                                                                                                   SEQUENCE FROM N.A.
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Archaea: Euryarchaeota; M
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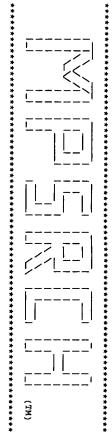
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii."; Science 273:1058-1073(1996).
-! - CATALYIIC ACTIVITY: 5-AMINO-6-(5-PHOSPHORIBITYLAMINO)URACIL + NADPH.
-NADP(+) = 5-AMINO-6-(5-PHOSPHORIBOSYLAMINO)URACIL + NADPH.
-! - PATHWAY: THIRD STEP OF RIBOFLAVIN BIOSYNTHESIS.
-! - SIMILARITY: BELONGS TO THE HTP REDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISAM: MODOST, Ribb_C; 1.
Hypothetical protein; Riboflavin biosynthesis; Oxidoreductase; NADP. SEQUENCE 224 AA; 25037 MW; 4D8C15CE291E89DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54; DB 1; Length 224;
Pred. No. 2.44e+00;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U67514; AAB98665.1; -.
TIGR; MJ0671; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.3%;
Best Local Similarity 33.3%;
Matches 6; Conservative
```

Search completed: Wed Sep $6\ 08:15:32\ 2000$ Job time : $12\ secs$.

118 ILEDMGVEVVKCGRGKVD 135

do yo

1 VIDHQGTKSSKCVRQKVE 18



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:15:49 2000; MasPar time 6.73 Seconds 216.433 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-08-487-283A-1 (1-21) from US08487283A.pep 141

Sequence: 1 VIDHQGTKSSKCVRQKVEGSS 21

Scoring table: PAM 150 Gap 15

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb112
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_nammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 25.849; Variance 31.531; scale 0.820

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11	Result
55 55 55 55 55 55 55 55 55 55 55 55 55	Score
48.14.44.44.44.44.44.44.44.44.44.44.44.44.	% Query Match
936 936 5213 213 211 214 1166 943 943 943 225 953 963 972 236 236	Length
110 110 110 110 111 111 111 111 111 111	BB
Q9XXXX Q9XXXX Q9XYXX Q9XYXX Q9XYXX Q9XYXX Q55550 Q55550 Q64645 Q64645 Q64645 Q60952 Q60952 Q60952 Q60952 Q60969 Q60970 Q70852 Q60969 Q60970 Q60462 Q66614 Q2	IJ
PUTATIVE CYTOCHROME C- CYTOCHROME C BIOGENESI PUTATIVE PROTEASE. TRANSCRIPTION FACTOR S HYPOTHETICAL 22.7 KD P MADS BOX PROTEIN AGL20 HYPOTHETICAL 139.4 KD LACTOPERRIN BINDING PR LACTOPERRIN RECEPFOR P ROTEIN TYROSINE PHOSP PROTEIN TYROSINE PHOSP PROTEIN TYROSINE PHOSP PROTEIN TYROSINE PHOSP PROTEIN TYROSINE PHOSP PROTEIN. FIBROBLAST GROWTH FACT KIAAO724 PROTEIN. GLOBULIN-1 (FRAGMENT). GLOBULIN-1 (FRAGMENT). GLOBULIN-1 (FRAGMENT).	Description
8, 98e-01 1, 21e-01 2, 00e-01 3, 31e-01 2, 00e-01 3, 44e-01 8, 88e-01 1, 44e+00 1, 44e+00	Pred. No.

4.4	43	42	41	40	39	38	37	36	ω	34	33	32	31	30	29	28	27	26	25	24	23	22	21
5 5 4 4	54	54	54	54	54	55	55	55	55	55	55	55	55	55	56	56	56	56	56	56	56	56	56
38.3 38.3									39.0	39.0	39.0	39.0	39.0	39.0	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7
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LYSINE SPECIFIC CYSTEI CELL SURFACE PROTEIN.	LYSINE-SPECIFIC CYSTEI	TONB-LINKED ADHESIN PR	CHROMOSOME XV READING	MADS BOX PROTEIN.	M79 PROTEIN.	POLYPROTEIN PRECURSOR.	NUP32D.	NUCLEOPORIN.	NUCLEOPORIN.	MAJOR OUTER CAPSID PRO	LAMIN.	CC4.3 PROTEIN.	IN ACYL-COA	NVERS	H	GLOBULIN-1 S ALLELE PR	CORONIN.	GLOBULIN1.	<u> </u>	GLOBULIN-1 (FRAGMENT).	GLOBULIN-1 (FRAGMENT).	_	GLOBULIN-1 (FRAGMENT).
	9.52e+00					6.00e+00	6.00e+00		6.00e+00		6.00e+00		6.00e+00	6.00e+00		3.75e+00	3.75e+00	•		3.75e+00	3.75e+00	3.75e+00	3.75e+00

ALIGNMENTS

OS DE	Db Qy RESULT	% å ℃	SORERRE	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2888	RESULT AC Q DT 00 DT 00 DT 0
O25141 PRELIMINARY; PRT; 936 AA. O25141; O1-JAN-1998 (TrEMBLrel. 05, Created) O1-JAN-1998 (TrEMBLrel. 05, Last sequence update) O1-NOV-1999 (TrEMBLrel. 12, Last annotation update) CTTOCHROME C BIOGENESIS PROTEIN (YCF5). HP0378. Helicobacter pylori (Campylobacter pylori).	366 IDMHGGKSAKIERQKIENPA 385 : : : :: 2 IDHQGTKSSKCVRQKVEGSS 21 ILT 2	Query Match 48.2%; Score 68; DB 2; Length 936; Best Local Similarity 50.0%; Pred. No. 8.98e-03; Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;	"Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori."; Nature 397:176-180(1999). EMBL; AE001528; AAD06582.1; SEQUENCE 936 AA; 106452 MW; A43D80C0 CRC32;	SEQUENCE FROM N.A. STRAIN-J99; MEDLINE; 99120557. ALM R.A., LING LS.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C., ALM R.A., LING LS.L., MOIR D.T., KING B.L., CARMEL G., SMITH D.R., NCONAN B., GUILD B.C., DEJONGE B.L., CARMEL G., TUMMINO P.J., CARUSO A., URIA-NICKELSEN M., MILLS D.M., IVES C., GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOVIS G.F., TRICT T.I.	Helicobacter pylori J99. Helicobacter pylori J99. Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter.	OPERDS PRELIMINARY; PRT; 936 AA. QPERDS; QPERDS; O1-MAY-1999 (TrEMBLrel. 10, Created) O1-MAY-1999 (TrEMBLrel. 10, Last sequence update) O1-MAY-1999 (TrEMBLrel. 10, Last annotation update) PUTARILY CYTOCHROME C-TYPE BIOGENESIS PROTEIN.

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MEDIME: 97077349.
MENZEL G., APEL K., MELZER S.;
"Identification of two MADS box genes that are expressed in the apical meristem of the long-day plant Sinapis alba in transition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KANEKO T., TANAKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N., SUGIURA M., TABATA S.;
SUGIURA M., TABATA S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                       Sinapis alba (White mustard) (Brassica hirta).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              flowering.";

Plant J. 9:399 408(1996).

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SIMILARITY: CONTAINS A DOMAIN FOUND IN SRF-TYPE TRANSCRIPTION EMBL; U2569; AAB41526.1;

HSSP; P11746; INMX.

MENDEL; 105511; Sinal: MADS:10511.

PRAM; PF001486; K-box; 1.

PFAM; PF001486; K-box; 1.

PFAM; PF001319; SRF-TF: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63; DB 10; Length 213;
Pred. No. 1.21e-01;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TABATA S.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation, DNA-binding, Nuclear protein. SEQUENCE 213 AA, 24408 MW; 0562BB62 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 02, Last annotation update)
HYPOTHETICAL 22.7 KD PROTEIN.
Synechocystis sp. (strain PCC 6803).
                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
TRANSCRIPTION FACTOR SAMADS A.
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                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=INFLORESCENCE MERISTEMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0404; MADSDOMAIN.
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504 HTGYASSKCVHRKVD 518
                                                                                                                            PRELIMINARY;
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                     | | | ||||||::||:
4 HQGTKSSKCVRQKVE 18
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Best Local Similarity
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MEDLINE; 96127529.
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Q55550
Q55550;
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OLIVER K., HARRIS D.;
"A set of commids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J., KINASHI H., HOPWOOD D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL049863; CAB42961.1; -.
                                                                                                                     TOME J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-F., GILL S., DOUGHERTY B.A.,
NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A.,
MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
COTTON M.D., WEIDNAN J.M., FUJII C., BOWANN C., WATTHEY L., WALLIN E.,
HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                   The complete genome sequence of the gastric pathogen Helicobacter
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces
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Pred. No. 7.25e-02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 65; DB 2; Length 936;
Pred. No. 4.33e-02;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=A3(2);
JAMES K.D., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical profein.
SEQUENCE 936 AA; 106359 MW; F1D27C55 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543 AA; 57696 MW; 0F49E825 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                        Nature 388:539-547(1997).
EMBL; AE000554; AAD07446.1; -.
TIGR; HP0378; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 IDMHGGKSAKIERQSVENSA 385
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Best Local Similarity 60.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         PF01578; CytC_asm; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 46.1%;
Local Similarity 55.0%;
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                        MEDLINE; 97394467.
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                                                          SEQUENCE FROM N.A.
                     Helicobacter
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                                                                                  STRAIN-26695
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Q9X7U3;

DATE OF THE SECTION O

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RESULT

Matches

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RESULT

ID 064645;

AC 064645;

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AC 064645;

AC 01-AUG-1998 (TTEMBLrel. 07, CIDT 01-AUG-1998 (TTEMBLrel. 12, Le DT 01-NOV-1999 (TTEMBLR)

DT 01-NOV-1999 (TTEMBLR)

MADS BOX PROTEIN AGL20.

GN MADS OR F17K2.19.

GN MADS OR F17K2.19.

GN MADS OR F17K2.19.

GN MADS OR F17K2.19.

CO Eukaryota; Viridiplantae; Streece eudicots; Rosidae; eurosicots; Euro
RESULT 7
ID 096219
AC 096219;
DT 01-MAY-1999
DT 01-MAY-1999
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Best Local Similarity
Matches 7; Conser
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Best Local (
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SEQUENCE FROM N.A.
STRAIN-PCC6803;
STRAIN-PCC6803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. COLUMBIA;
ROUNSLEY S.D., KAUL S., LIN X., KETCHUM K.A., CROSBY M.L
BRANDON R.C., SYKES S.M., MASON T.M., KERLAVAGE A.R., AD
SOMERVILLE C.R., VENTER J.C.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions." DNA Res. 3:109-136(1996).
EMBL: D63999; BAA10048.1; -.
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KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKA KANEKO T., SATO S., KIMURA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., Y
                                                                                                                                                                                                                                                                                                                                                                                                                                   MENDEL; 29412; Arath; MADS; 29412.
PROSITE; PS00350; MADS_BOX_1; 1.
PFAM; PF01486; K-box; 1.
PFAM; PF00319; SRF-TF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein. SEQUENCE 213 AA; 22745 MW;
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1 VIDHQGTKSSKCVRQKVEGS
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L; AC003680; AAC06175.1; -.
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                                                                                                                                                                         IDHOGTKSSKCVRQK
  (TrEMBLrel.
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larity 46.7%;
Conservative
                                                                          PRELIMINARY;
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Last sequence update)
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Pred. No. 3.31e-01;
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  sequence update)
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FOUND IN SRF-TY
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2.00e-01;
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Best Local S
Matches
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Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                          087343
087343;
087343;
01-NOV-1998
01-NOV-1998
01-MAY-1999
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Q51187;
Q51187;
01-NOV-1996
01-NOV-1996
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Bacteria;
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Plasmodium
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EMBL; X79838; CAA56233.1; -.
PFAM; PF00593; TonB_boxC; 1.
   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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"Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.";
                                                                                                                                                        LBPA
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EMBL; AECO1407; AAC71915.1; -.
Hypothetical protein.
SEQUENCE 1166 AA; 139389 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (
                                                                                                                                                                                               LACTOFERRIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular characterization of the structural receptor of the meningococcal strain H44/76.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PETTERSSON A.M., KLARENBEEK V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 95272374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               592 RSRKCVPRKINGSN : | | | | : | : : | | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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Similarity 43.8%;
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                                                                              Proteobacteria;
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8 (TrEMBLrel. 08,
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N BINDING PROTEIN
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L 139.4 KD P
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rel. 01,
rel. 08,
PROTEIN.
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Pred. No.
5; Misma
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A PRECURSOR.
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No. 5.44e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59; DB 2;
No. 8.88e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemosporida;
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SEQUENCE FROM N.A.
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060970;
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P71852
P71852;
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       MEDLINE; 98261564.

LEWIS L.A., ROHDE K., GIPSON M., BEHRENS B., GRAY E., TOTH S.I.,

LEWIS L.A., DYER D.W.;

"Identification and molecular analysis of lbpBA, which encodes the

two-component meningococcal lactoferrin receptor.";

Infect. Immun. 66:3017-3023(1998).

EMBL; AF049349; AAC35271.1;

PERMI, PF00593; TONB_boxC; 1.
                                                                                                                                                                                                                                                                                                                                                          STRAINSFAIS;
MEDLINE: 95347808.
BISWAS GO.D., SPARLING P.F.;
Ficharacterization of lbpA, the structural gene for a lactoferrin receptor in Neisseria gonorrhoeae.";
Infect. Immun. 63:2958-2967(1995).
-!- SIMILARITY: STRONG, TO N.MENINGITIDIS IRON-REGULATED OUTER MEMBRANE PROTEIN A.
EMBL: 016260; AAC13780.1; -.
PFAM: PF00593: TonB_boxC; 1.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1999 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TREMBLrel. 12, Last annotation update)
NOV-1999 (TREMBLrel. 12, Last annotation update)
Mus musculus (Mouse).
ENGRATYOTA: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                            LACTOFERRIN BINDING PROTEIN A. 1; 087E2FC6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59; DB 2; Length 943;
Pred. No. 8.88e-01;
5; Mismatches 2; Indels
                                                                                                                                         Score 59; DB 2; Length 943;
Pred. No. 8.88e-01;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LACTOFERRIN RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LACTOFERRIN RECEPTOR.
                                                                                                                                                                                                                                                 943 AA
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24 943 LAO
943 AA; 105426 MW;
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25 943 LA
943 AA; 105669 MW;
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Similarity 50.0%;
7; Conservative
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                                                                                                                                                    Similarity 50.0%; 7; Conservative
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TISSUE-SKELETAL MUSCLE;
MEDLINE; 96070766.
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Best Local Similarity
Matches 7; Conser
                                                                                                                                                     Best Local Similarity Matches 7; Conser
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STRAIN=DNM2
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                                                                                                                                           Query Match
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Q50952
Q50952;
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SIGNAL
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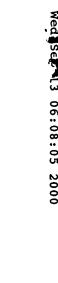
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MEDLINE; 96070766.
WISHART M.J. DENU J.M., WILLIAMS J.A., DIXON J.E.;
WISHART M.J. DENU J.M., WILLIAMS J.A., DIXON J.E.;
WISHART M.J., DENU J.M., WILLIAMS J.A., DIXON J.E.;
WISHART M.J., DENU J.M., WILLIAMS J.A., DIXON J.E.;
J. Baiol. Chem. 270:26782-26785(1995).
EMBL; U34913; AAAR37037.1; -.
HSSP; P31452; JVHR.
PFAM; PF00782; DSPC; 1.
SEQUENCE 223 AA; 25416 MW; 7D7F6D83 CRC32;
WISHART M.J., DENU J.M., WILLIAMS J.A., DIXON J.E.;
"A single mutation converts a novel phosphotyrosine binding domain into a dual-specificity phosphatase.";
J. Biol. Chem. 270:26782-26785(1995).
EMBL; U34973; AAA87036.1; -..
EMBL; U34973; AAA87036.1; -..
PFRAM; PF00782; DSPC; I. SEQUENCE 205 AA; 23683 MW; 7B70331A CRC32;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PROTEIN TYROSINE PHOSPHATASE-LIKE.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Rodenta; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                Length 205;
                                                                                                                                                                                                                                                                                                                                        6; Indels
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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BARRELL B.G., RAJANDREAM M.A.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-ROV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 26.8 KD PROTEIN.
                                                                                                                                                                                                                                                                          Query Match
41.1%; Score 58; DB 11; I
Best Local Similarity 25.0%; Pred. No. 1.44e+00;
Matches 5; Conservative 9; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                       51 ILQKHGITHIICIRQNIEAN 70
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RESULT 14

ID P90814; P90875; P91838;
AC P90814; P90875; P91838;
DT 01-MAY-1997 (TIEMBLITE1 03
DT 01-MAY-1999 (TIEMBLITE1 04)
DE F46C5.9; OC ELWAITYOTA; Metazoa; Nemato OC ELWAITYOTA; MAJORE FROM N.A.

RA LIGHTNING J., BURTON J., CO RA CARATON M., DARR S., DU Z.
RA GARDNER A., GREEN P., HAWK RA GARDNER A., GREEN P., HAWK RA GARDNER A., WEINSTOCK L., WE RISTOR THERY-MIEG J., THOMAS K.
RA WAITSON A., WEINSTOCK L., WE PARSONS J., PERCY C., MC RA TIERA J., PERCY C., MC RA PARSONS J., PERCY C., MC J., PE
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Best Local S
Matches
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EMBL; Z82098; CAB05057.1; -.
HSSP; P29132; lDFI.
PFAM; PF00106; adh_short; 1.
PFAM; PF000678; adh_short_C2; 1.
PRINTS; PR00080; ALCDHDRGNASE.
PRINTS; PR00081; GDHRDH.
                                                                                                                                                                                                                                                                                                                                                                                                 WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2 2 Mb of contiguous nucleotide sequence from chromosome III of C elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditina; Rhabditoidea;
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MEDLINE; 96181548.
PHILIPP W.J., POUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. SEQUENCE 259 AA; 2
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VIDHQGTKSSKCVRQKVEG
  CAB05407.1;
CAB05407.1;
CAB05407.1;
CAA91052.1;
CAA91052.1;
CAA91052.1;
CAA91052.1;
CAA91052.1;
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AN V., HEYM
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Pred. No. 1.44e+00;
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Q26614;
Q16614;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
FIBROBLAST GROWTH FACTOR RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                       CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCCOON P.E., ANGERER L.M., Submitted (NOV-1994) to the EMBL; U17164; AAC47258.1; HSSP; P08631; 2HCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strongylocentrotus purpuratus (Purple sea urchin). Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea; Euechinoidea; Echinoidea; Echinoidea; Echinoidea;
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EMBL; 283016; CAA92666.1;
PFAM; PF00400; WD40; 2.
SEQUENCE 451 AA; 50881
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Pred. No.
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Pred. No. 1.44e+00;
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FIBROBLAST GROWTH
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1. No. 1.44e+00;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Wed Sep 6 08:17:17 2000; MasPar time 2.98 Seconds 166.869 Million cell updates/sec

Tabular output not generated.

Description: Perfect Scor >US-08-487-283A-1 (1-21) from US08487283A.pep

Score:

Sequence: 1 VIDHQGTKSSKCVRQKVEGSS 21

Scoring table: PAM 150 Gap 15

188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 18.949; Variance 55.942; scale 0.339

d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
114 144 155 155 155 155 155 155 155 155	Score
100 0 400 0 100 0 39 0 39 3 38 3 38 3 38 3 37 6 37 6 37 6 37 6 37 6 37 6 37 6 37	Query Match
11732 1732 1732 1732 1732 1732 1732 1732	Length
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	BB
R77605 R77604 Y07037 R22271 R840449 W840487 W84787 W24787 W24787 W24787 W24787 W24787 W85474 W85474 R861124 R861124 R86206 R08267 R86206 R08267 W65762 W6576	ID
Pro-C5 polypeptide KSS pro-C5 polypeptide. Breast cancer associat CSHase. Rice OsMADS7 protein 1 Haemagglutinin protein protei	Description
1.94e-09 3.93e+01 6.46e+01 8.26e+01 8.26e+01 8.26e+01 1.05e+02 1.05e+02 1.05e+02 1.05e+02 1.05e+02 1.05e+02 1.05e+02 1.34e+02 1.34e+02 1.34e+02 1.34e+02 1.34e+02 1.34e+02 1.34e+02	Pred. No.

R77604 standard; Protein; 1676 AA.
R77604;
15-MAR-1996 (first entry)
Pro-C5 polypeptide.
Complement C5; haemolysis; kidney; glomerulonephritis;
monoclonal antibody; antiinflammatory; antibody engineering;

45	44	43	42	41	40	39	38	37	36	35	34	33	32	μ	30	29	28	27	26	25	24
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_	Sugarbeet choline mono	Flavobacterium keratol	H. pylori GHPO 37 prot	Plasmodium falciparum	Malarial PfEMP3 epitop	Tobacco mosaic virus r	Tobacco mosaic virus r	Murine JAK2 kinase.	B.thuringiensis toxin/	JAK2.		B.thuringiensis toxin/	Enterococcus faecalis	댦	Rat neurodap 1 protein	A. thaliana protein co	A. thaliana SGT protei	Rat epithelin precurso	Baculovirus ISP protei	Autographa californica	Zea mays antimicrobial
2.17e+02	2.17e+02	2.17e+02	2.17e+02	1.71e+02	1.71e+02	1.71e+02	1.71e+02	1.71e+02	1.71e+02	1.71e+02	1.71e+02	1.71e+02	1.71e+02	1.71e+02	1.71e+02	1.71e+02	1.71e+02	1.71e+02	1.71e+02	1.71e+02	1.34e+02

ALIGNMENTS

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Matches 2
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01-MAY-1995; U05688.
02-MAY-1994; US-236208.
02-MAY-1994; US-236208.
(ALEX-) ALEXION PHARM INC.
(ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating glomerulonephritis with antibody against complement C5 component - to inhibit complement induced cell lysis Example 13; Page 81; 181pp; English.

The cDNA sequence of the complement C5 gene transcript predicts a secreted pro-C5 precursor of 1676 amino acids (R77604). C5 is a beta-globulin heterodimer thought to play a role in the pathogenesis of glomerulonephritis (GN). Cleavage of the C5 alpha-chain by a convertase enzyme generates anaphylatoxic C5a. Monoclonal and humanised recombinant antibodies that recognise the alpha-chain KSSKC epitope (R77605) block C5a generation, thereby reducing glomerular inflammation and kidney dysfunction associated with GN. Sequence 21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pro-C5 polypeptide KSSKC epitope.
Complement C5; haemolysis; kidney; glomerulonephritis;
monoclonal antibody; antiinflammatory; antibody engineering;
humanised antibody; KSSKC epitope.
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WO9529697-A1.
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Similarity 100.0%;
21; Conservative
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Pred. No. 1.94e-09;
0; Mismatches 0;
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LT 5
W84049 standard; Protein; 249 AA.
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                    11-OCT-1997; GB-021697
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Breast cancer associated antigen precursor sequence.
Cancer associated antigen; diagnosis; research; treatment; human;
breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating glomerulonephritis with antibody against complement C5 component - to inhibit complement induced cell lysis Example 13; Page 82-92; 181pp; English.

The cDNA sequence of the complement C5 gene transcript predicts a secreted pro-C5 precursor of 1676 amino acids (R77604). C5 is a beta-globulin heterodimer thought to play a role in the pathogenesis of glomerulonephritis (GN). Cleavage of the C5 alpha-chain by a convertase enzyme generates anaphylatoxic C5a. Monoclonal and humanised recombinant antibodies that recognise the alpha-chain KSSKC epitope (R77605) block C5a generation, thereby reducing glomerular inflammation and kidney dysfunction associated with GN.
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                                                                                                                                                                                                            678. 1676
/label- Alpha-chain
/note- "amino acids 872-892 (854-874 of
the mature protein) comprise the KSSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S
Rother RP, Springhorn J P, Squinto SP, Thomas TC;
WPI; 95-392923/50.
                                                                                                                                                                                                                                                                                            epitope"
678. 751
/label= C5a
751. 752
/label= Convertase_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1630
/label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                  'label - N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                         label - N-glycosylation_site
                                                                                         19. .673
/label= Beta-chain
673. .674
674. .677
label= Cleavage_peptide
                                                       1. 18
/label= Sig_peptide
                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r 3
Y07037 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      872 VIDHQGTKSSKCVRQKVEGSS 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VIDHQGTKSSKCVRQKVEGSS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1995; U05688.
02-MAY-1994; US-236208.
(ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-1998; US-102322.
17-JUL-1997; US-896164.
10-OCT-1997; US-061599.
10-OCT-1997; US-061765.
                                                                                                                                                                                                                                                                                                                                                                                                                                         1115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1676 AA;
humanised antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer.
                                                                                                                                      cleavage_site
                                                                                                                                                           cleavage_site
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WO9904265-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09529697-A1
                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                         peptide
                                                                                                protein
                                                                                                                                                                             peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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WPI: 99-132448/11.

New isolated cancer associated nucleic acids and polypeptides -
isolated using sera from cancer patients, used to develop products

PT isolated using sera from cancer patients, used to develop products

for the diagnosis, monitoring or treatment of cancers

Disclosure; Page 422; 787pp; English.

Disclosure; Page 422; 787pp; English.

CT he invention relates to a method for diagnosing a disorder characterised

CT he invention relates to a method for diagnosing a precursor coded for by

a nucleic acid molecule (NAM). The method comprises: (a) contacting a

CT blological sample isolated from a subject with an agent that specifically

CT binds to the NAM, an expression product or a fragment of an expression

CT product complexed with an HIAA molecule; and (b) determining the

CT product complexed with an HIAA molecule; and (b) determining the

CT chermination of the disorder. The products and methods can be used in

CT chermination of the disorder. The products and methods can be used in

CT characterised by the expression of various cancer associated antigens.

CT characterised by the expression of various cancer associated antigens.

CT characterised by the expression precursors expressed in human breast

CT cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful in clinical assay of creatinine, and vectors providing efficient expression in E.coli claim 9; page 9 + 7; 12pp; German. The sequence encoding CSHase is useful in assay of creatinine (for diagnosis of kidney disease). It can now be prepd. more simply than by known methods which involve culture of Arthrobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burtscher H, Schumacher G;
WPI; 92-098378/13.
W-PSDB; Q22713.
Recombinant DNA encoding N-carbamoyl-sarcosine-amidohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB 1; Length 117;
Pred. No. 3.93e+01;
6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55; DB 1; Length 264; Pred. No. 6.46e+01; 4; Mismatches 3; Indels
(LUDW-) LUDWIG INST CANCER RES.
Chen Y, Gout I, Gure A, OHare M, Obata Y, Old LJ,
Pfreundschuh M, Sahin U, Scanlan MJ, Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-WAR-1992.
19-SEP-1991; 115974.
20-SEP-1990; DE-029844.
(BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R22271 standard; Protein; 264 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 40.4%;
Best Local Similarity 41.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.08;
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6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUL-1992 (first entry) CSHase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arthrobacter sp. DSM 2563
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Best Local &
Matches
                                                                                                                                                                             US5824791-A.
20-CCT-1998.
11-DEC-1995; 570311.
11-DEC-1995; US-570311.
08-SEP-1988; US-241640.
25-JAN-1991; US-35485.
CUABR-) UAB RES FOUND.
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03-DEC-1998.
02-JUN-1998; U11278.
02-JUN-1997; US-867087.
(UNIW ) UNIV WASHINGTON S
     Isolated Porphyromonas gingivalis genes - encoding haemagglutinin and/or protease poly:peptide(s))
Claim 1; Column 69-84; 101pp; English.
This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the prtp haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and periodontal disease.
                                                                                                                                                                                                                                                                                Haemaggiutinin protein pitP.
Porphyromonas gingivalis.
US5824791-A
                                                                                                                                                                                                                                                                                                                                                                    LT 6
W69487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated CDNA clone (see V71740). OSMAD7 is a novel MADS-box gene involved in the control of floral development and apical dominance. OSMADS6 (see W84048) and OSMADS6 (see W84050) proteins are also disclosed. Expression of OSMADS6 (see W84050) proteins are also transgenic plant causes the plant to exhibit at least one phenotype selected from: (i) diminished apical dominance, (ii) early flowering, (iii) altered daylength requirement for flowering, (iv) greater synchronisation of flowering, and (v) relaxed vernalisation requirement, compared to a non-transgenic control plant. Claimed methods of producing such a transgenic plant utilise: (i) OSMADS6, OSMADS7 or OSMADS8 nucleic acids (see V71739-41).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New plant MADS-box genes - useful for, development and apical dominance Example 1; Fig 2; 53pp; English. This is the amino acid sequence of rice
                                                                                                               WPI; 98-582627/49.
N-PSDB; V58874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-1999 (first entry)
Rice OsMADS7 protein involved in floral development.
OsMADS7; rice; flower development; apical dominance;
transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                           Tumwasorn
                                                                                                                                                      Han N, Lantz M, Lepine G,
                                                                                                                                                                                                                                                                                                                                     22-DEC-1998 (first entry)
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15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                    160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                       DHQGTKSSKCVRQKVEGSS
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                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                     UNIV FLORIDA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249
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larity 26.3%;
Conservative
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95. .159
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2. .57
                                                                                                                                                                                                                                                                                                                                                                 Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE
                                                                                                                                                                                                                                                                                                                                                                  1732
                                                                                                                                                      Patti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                  ξ
 genes
                                                                                                                                                      'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 8.26e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rice OsMADS7, as deduced from a OsMAD7 is a novel MADS-box gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for, e.g. controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apical dominance; dwarfism;
                                                                                                                                                     Progulske-Fox
                                                                                                                                                                                                                                                                                                          disease; vaccine;
polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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SACTOR SEPTEMENT FOR THE PROPERTY OF THE PROPE
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                                CA PrtR-PrtK cell surface protein of Porphyromonas ginivalis (PG)
Comprises a 300 kDa complex composed a 48 kDa lysine-specific
Child protease and 39, 15 and 44 kDa adhesins encoded by the prtK
C gene (T78851), and a 45 kDa arginine-specific thiol protease and
C 44, 15, 17 and 27 kDa adhesins (see W24786) encoded by the prtR
C gene (T78850). A claimed antigenic complex comprises at least one
c multimeric protein complex of PrtR and PrtK each containing at
C least one adhesin domain, the complex having a mol.wt. of over 200
C kDa, and preferably comprises all 9 proteins of the PrtR-PrtK
C complex (see also W24780 85). It can be used in a claimed
C composition to elicit an immune response directed against PG, and
C compestition to elicit an immune response directed against pG, and
C in a claimed method of reducing the prospect of FG infection and/or
C severity of disease. Antibodies directed against the complex are
C claimed for use in treating PG infection. Unlike whole PG cells or
C capsule, the PrtR-PrtK complex or component parts are safe and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
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W24787;
W24787;
25-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antigenic protein complex from Porpl
comprising Arg- and Lys- specific thiol
the detection, prevention and treatment
Example 1; Fig 9b; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PrtK antigenic protein complex.
Periodontal disease; cell surface protein; thiol endopeptidase; PrtK; PrtK48; PrtK39; PrtK15; Prth haemaggluthin; adhesin; therapy; diagnosis; vacc Porphyromonas gingivalis strain W50.
                          effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYME) UNIV MELBOURNE.
(VICT-) VICTORIAN DAIRY
Bhogal PS, Reynolds EC,
WPI; 97-272112/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cleavage_site
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cleavage_site
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Sequence 1732 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; T78851.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein; 1732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 31.6%, 6; Conservative
  antigens.
1732 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AU0673.
AU-006275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "15 kDa a
1291 .1292
1292 .1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "39 k
1156. .1157
1157. .1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- Prti
/note- "48 )
737. .738
738. .1156
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/label- P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Pro-pro_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complex from Porphyromonas gingivalis -
ys- specific thiol endo-peptidase(s), us
tion_and_treatment of periodontal diseas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IND AUTHORITY
, Slakeski N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PrtK44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PrtK39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PrtK48
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Pred. No.
7; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adhesin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adhesin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adhesin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lys-specific thiol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; DB 1; I
. 8.26e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease
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Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine;
                                                                                                                                                                                                    WO9521922-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simons JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Porphyromonas gingivalis genes and proteins - used in the detection
                                                                                                                                                                                                                                                                                            P. gingivalis porphypain.
Porphypain; haemagglutinin; periodontal disease; vaccine; antibody.
Porphyromonas gingivalis strain W12.
Rey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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94347;
R94347;
02-JUL-1996 (first entry)
Hepatitis GB virus (HGBV) clone GB contig A protein prod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.3%; Score 54; DB 1; Length 1732
31.6%; Pred. No. 8.26e+01;
7. Wismatches 6; Indels
Best Local Similarity 31.6%; Pred. No. 8.26e+01;
Matches 6; Conservative 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lantz M, Lepine G, Patti JM, Progulske-Fox A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1341. .1405
/note= "Pro-Asn repeat region type 2"
1430. .1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  887. .952
/note= "Pro-Asn repeat region type 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              type 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Pro-Asn repeat region type 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              946. 967
/note-"Pro-Asn repeat region 7.00te-"Pro-Asn repeat region 7.00te-"Pro-Asn repeat region to 1041. 1100
                                                                                                                                                                                                                                                                                                                                                                                                   688. .708
/note= "Pro-Asn repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1430. 1451
/note= "Pro-Asn repeat region
1488. 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1041. .1100
/note= "Pro-Asn repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Pro-Asn repeat region
1607. .1650
                                                                                                                                                                                               .r 8
R96029 standard; Protein; 1732 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1097 ITAKGVRSPKAIRGRIQGT 1115
                                                                        1097 ITAKGVRSPKAIRGRIQGT 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 IDHQGTKSSKCVRQKVEGS 20
                                                                                                    2 IDHQGTKSSKCVRQKVEGS 20
                                                                                                                                                                                                                                                                            04-SEP-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUN-1996.
11-DEC-1995; U16108.
09-DEC-1994; US-353485.
(UARP.) TAB RES FOUND.
(UYEL) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 96-287181/29.
N-PSDB; T30653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9617936-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
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Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful for diagnosis and therapy of hepatitis GB virus

Example 9; Pages 401-414; 661pp; English.

Double stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV

confected tamarin plasma, using standard procedures, was used to prepare a lambda phage HGBV conversed rescued from the lambda phage, searched against a sequence database and from the lambda phage, searched against a sequence database and assemble the sequences. The clones were then used to assemble the sequences 70129/30 (GB contig A and B) which encode the proteins R94345-47 (the 3 possible coding strand reading frames) and R82072, respectively. Reagents which comprise the HGBV or its procein prods. can be used for the diagnosis, therapy sequence 3163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
reagents; non-A; non-B; non-C; non-D; non-E; clone; GB contig A; tamarin; infected plasma; lambda phage; cDNA library. Hepatitis GB virus.
                                                                                                  misc_difference 1. .3163
./note= "others correspond to degenerate or STOP codons in T00129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                Buijk SL, Dawson GJ, Desai SM, Erker JC, Leary TP;
Muerhoff AS, Mushahwar IK, Pilot-Matias TJ, Schlauder GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54; DB 1; Le
Pred. No. 8.26e+01;
5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R14327;
17-JAN-1992 (first entry)
Mouse epithelin precursor.
Fr. growth regulation; inhibition; stimulation.
Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= EP-2
/note= "claim 23, page 55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "claim 26, page 56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "claim 24, page 55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              claim 24, page
.123. .179
/label= EP
/note= "claim 25, page 55
362. .416
/nabel= EP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280. .335
/label= EP-1
/note= "claim 22, page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .589
/label= precursor
/note= "claim 21, pag
280. .335
                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 10
R14327 standard; Protein; 589 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59. .114
/label= EP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .261
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                                                                                                                                                                                                                                                 14-FEB-1994; US-196030.
13-MAY-1994; US-242664.
29-JUL-1994; US-28314.
23-NOY-1994; US-344190.
23-NOY-1995; US-344185.
27-JAN-1995; US-344557.
(ABBO ) ABBOTT LAB.
Buijk SL, Dawson GJ, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VIDHQGTKSSKCVRQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 6; Conser
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TRESULTATION OF THE PROPERTY O
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9115510-A.
17-OCT-1991; U02321.
03-APR-1990; US-504508.
13-MAR-1991; US-083796.
(BRIM ) BRISTOL-MYERS SQU
Shoyab M, PLOWMAN GD;
WPI; 91-325168/44.
                                                                                                                                                                                                                                              26-NOV-1998.

22-MAY-1998; U10555.

22-MAY-1997; US-991862.

23-MAY-1997; US-963079.

(SERR/) SERRERO G.

SETTETO G:
                                                                                                          N-PSDB; V82824

Composition containing antagonist of growth
composition containing antagonist of growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis

place of the protein prote
treating cancer and viral diseases and also for diagnosing from altered GP88 expression Example 5; Fig 8A-D; 86pp; English. This is the amino acid sequence of murine GP88, an 88 kDa glycoprotein autocrine growth factor and epithilin/granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse GP88 autocrine growth factor.

GP88; granulin; epithilin; mouse; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity.

See also Q14338-40, Q14952-53, R14328-9 and R15315-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 11
W85474 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9852607-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                              99-045276/04.
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/label= EP
/note= "claim;
515. .570
/label= EP
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562. .!
/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "S14R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "K19T peptide, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "P12T
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Pred. No. 1.05e+
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by CTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by AGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to raise antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ដ
                                                                                                                          factor GP88 - useful for for diagnosing disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                raise antibody"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                raise antibody'
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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.6%;
Best Local Similarity 35.7%;
Matches 5; Conservative
                                                                    09-FEB-1993 (
Type B human p
PDGF; PDGF-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-1995.
16-UN-1995; U07754.
17-UN-1994; US-261663.
(REGC) UNIV CALIFORNIA.
(USDA) US SEC OF AGRIC.
Baker BJ, Whitham SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Nicotiana glutinosa N gene tr
resistance to tobacco mosaic viru
coding for the protein was obtd.
library by transposon tagging. I
protein can be used to generate t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R88124
R88124;
                                                Homo sapiens.
                                                                                                                                                 R26206 standard; Protein; 1009 R26206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virus
Claim 28; Page 75-79; 98pp;
Claim 28; Page 75-79; 98pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tobacco mosaic virus resistance N gene truncated protein. Tobacco mosaic virus resistance; TMV; N gene; Solanaceae;
peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant virus resistance gene N sequence sequence of transgenic Solanaceous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             crop improvement; transgenic plant; crop improvement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor that is expressed in a tightly regulated manner in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; T09342.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicotiana glutinosa.
WO9535024-Al
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| :::::||:| |:
4 HQGTKSSKCVRQKV
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                                                                                                                                                                                                                                                                                                                           156 DNRDKTDADCIRQIVD
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 31.3% nes 5; Conservative
                                                                                                                                                                                                                                                                           ω
                                                                                                                                                                                                                                                                           DHQGTKSSKCVRQKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                platelet-derived growth
                                                                                                                          (first entry)
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                                                                         mesenchyme;
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Location/Qualifiers
1. .23
                                                                                                                                                                                                                                                                                                                                                                                                   37.6%;
                                                                                                                                                                                                                                                                                                                         171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene truncated protein aic virus (TMV). A cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            652
                                                                         tyrosine
                                                                                                                                                                                                                                                                                                                                                                         Pred.
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Pred.
7; N
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences from tobacco -
eous plants resistant to I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                          ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequences encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic plants, esp. Solanaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e 53; DB 1; Lens
1. No. 1.05e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us (TMV). A cDNA clone (T09342) from a N. glutinosa leaf cDNA DNA sequences encoding it.
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   No.
                                                                         kinase;
                                                               factor receptor.
inase; ligand binding region.
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                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                   .05e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 652
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Disclosure; Page 90: 109pp; English.

Disclosure; Page 90: 109pp; English.

The sequence given is one allele of type A human platelet-derived
The sequence given is one allele of type A human platelet-derived
The sequence given (PDGF R). This receptor is typically
found on cells of mesenchymal origin. It acts while in the form of
two transmembrane glycoproteins, each of which is about 180 kD.

This receptor has three major regions. The first is a transmembrane
region, which spans the membrane once, separating the regions of the
receptor exterior to the cell from those interior to the cell. The
second region is an extracellular region which contains the domains
which bind the PDGF. The third region is an intracellular region
which possess a tyrosine kinase activity. This tyrosine kinase
domain is notable in having an insert of approx. 100 amino acids,
as compared with most other receptor tyrosine kinase domains which
are contiguous or have shorter insert sequences. Fragments of this
sequence between 8 and 400 amino acids comprising one or more PDGF
Ligand a PDGF. Ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding platelet-derived growth factor - used to transform cells for culturing to detect PDG agonists and antagonists claim 1; Fig 1; 30pp; English.

Gene product may be expressed from a transformed cell. It has utility in dection of PDGF agonist and antagonist analogues, binding AA, AB and BB isoforms. PDGF agonists may be used to enhance wound healing, and antagonists may be used to block the effects of PDGF eg. in treatment of atherosclerosis or fibrotic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                             Platelet derived growth factor receptor (PDGF-R) poly:peptide(s) useful as therapeutic and diagnostic agents e.g. for assaying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                Escobedo JA, Fretto LJ, Giese NA, Tomlinson JE, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 53; DB 1; Length 1009;
Pred. No. 1.05e+02;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-1991 (first entry)
Platelet derived growth factor (PDGF) receptor protein.
Atherosclerosis; fibrotic diseases.
/label= Signal_peptide
                      24. .1009
/label= Mature_PDGF-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R08267 standard; protein; 1089 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381 VDDHHGSTGGQTVRCTAEGTP 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VIDHQGTKSSKCVRQKVEGSS 21
                                                                                                                11-JAN-1991; US-bours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 38.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-1990.
21-MAY-1990; U02849.
22-MAY-1989; US-355018.
(ZYMO-) ZYMOGENETICS INC.
                                                                                                     28-JAN-1992; U00730.
31-JAN-1991; US-650793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kelly JD, Murray MJ;
WPI; 90-375992/50.
N-PSDB; Q06869.
                                                                                                                                                                                                       WPI; 92-299970/36.
N-PSDB; 027451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
WO9014425-A.
                                                                W09213867-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                           protein
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16-JAN-1991 (first entry)
Alpha type PDGF receptor deduced from TR4 cDNA clone.
Platelet derived growth factor; Tl1.
                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                        R06910 standard; protein; 1089 AA.
R06910;
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label tyrosine autophosphorylation site 24. .524 /label=ligand binding domain 525. .548 /label-transmembrane region 549. .599 /label=juxtamembrane domain 600. .627 /label-ATP binding site 1. .23 /label-signal peptide /label=N-glycos_site 103. 105 /label=N-glycos_site 359. .361 /label-N-glycos_site 458. .460 /label-N-glycos_site 179. .181 /label=N-glycos_site 353. .355 -7abel=N-glycos_site 12. .44 /label=N-glycos_site /label-N-glycos_site modified_site modified_site modified_site modified_site modified_site modified_site modified_site modified_site modified_site Homo sapiens. binding_site WO9010013-A. domain domain domain domain

Matsui T, Aaronson SA, Pierce JH; WPI; 90-290306/38. N-PSDB; Q05989. (USDC) US SEC OF COMMERCE. 07-SEP-1990. 08-FEB-1990; U00617. 09-FEB-1989; US-308282.

Type alpha platelet-derived growth factor receptor gene - useful for transforming cells to express novel protein receptor and also

susceptible to generic engineering.

Claim 7; Fig 3: 64pp; English.

The TR4 clone is the largest contone related to the Til genomic clone, isolated from a library prepd. from human thymus DNA. The TR4 clone is the largest contone was isolated from a M426 human embryo fibroblast to DNA library.

The coding region can be introduced into the pSV2 gpt vector with a simian sarcoma virus LTR as a promoter and expressed in a host. The resulting protein is a novel PDGF creeptor designated type alpha (the known receptor is designated type beta). The polypeptide has a calculated molecular mass of 120 kb and has all the characteristics of a membrane spanning tyrosine type beta). The extracellular region comprises a hydrophobic signal peptide and a ligand binding domain which has structural compology with the PDGF-R/CSF1-R subfamily. Ten Cys residues are family and eight potential N-linked glycosylation sites are also present. A hydrophobic segment spans the membrane and the cytor plasmic region comprises a juxtamembrane region, a tyrosine kinase cegion split into TR1 and TR2 by a hydrophic interkinase region and a hydrophic segment spans the membrane and the cytor plasmic region comprises a juxtamembrane region includes the consensus ATP binding sequence (G-X-G-X-K-G. . R) and a tyrosine consensus ATP binding sequence (G-X-G-X-K-G. . R) and a tyrosine sequence consensus ATP binding sequence (G-X-G-X-K-G. . R) and a tyrosine consensus ATP binding sequence (G-X-G-X-K-G. . R) and a tyrosine consensus ATP binding sequence (G-X-G-X-K-G. . R) and a tyrosine consensus ATP binding sequence (G-X-G-X-K-G. . R) and a tyrosine consensus ATP binding sequence (G-X-G-X-K-G. . R) and a tyrosine consensus ATP binding sequence (G-X-G-X-K-G. . R) and a tyrosine consensus ATP binding sequence (G-X-G-X-K-G. . R) and a tyrosine consensus ATP binding sequence (G-X-G-X-K-G. . R) and a tyrosine consensus ATP binding sequence (G-X-G-X-K-G. . R) and a tyrosine consensus ATP binding sequence to that of pp60 (V-S-C.).

1089 AA;

Seguence

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Gaps

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.421 VDDHHGSTGGQTVRCTAEGTP 441

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:17:46 2000; MasPar time 2.27 Seconds 141.637 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-487-283A-1 (1-21) from US08487283A.pep 141 1 VIDHQGTKSSKCVRQKVEGSS 21

Scoring table: PAM 150 Gap 15

Searched: 152433 seqs, 15329240 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 17.928; Variance 54.211; scale 0.331

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222118776554 222128776554 22212877657	Result No.
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	Score
27.6668337.666837.666837.666837.666837.666837.666837.666837.666837.666837.666837.666837.666837.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.66687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6687.6	Query Match
944 944 24 24 1732 24 1732 1732 1089 589 589 589 1089 1089 1089 1089 1089	Length 1
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23, Applicati 24, Applicati 127, Applicati 128, Applicati 129, Applicati 130, Applicati 130, Applicati 130, Applicati 140, Applicati 150, Applicati 160, Applicati 170, App	ion
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## ALIGNMENTS

88888888	ននននន	38888888	888888888	8888888888	RESULT ID U XX AC X XX DT XX DE S XX
TELEPHONE: (416) 595-1155 TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 944 amino acids TYPE: amino acid STRANDEDNESS: single	ATTORNEY, AGENT INFORMATION:  NAME: Stewart, Michael I  REGISTRATION NUMBER: 24,973  REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb  TELECOMMUNICATION INFORMATION:		, M.S.	Sequence 23, Application US/08867941 Patent No. 5977337 GENERAL INFORMATION: APPLICANT: LOOSMOTE, Sheena M APPLICANT: Du, Run-Pan APPLICANT: Wang, Quijun APPLICANT: Wang, Yan-Ping APPLICANT: Yang, Yan-Ping APPLICANT: Klein, Michel H TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA NUMBER OF SEQUENCES: 67	LT 1 US-08-867-941-23 STANDARD; PRT; 944 AA.  xxxxxx  Sequence 23, Application US/08867941

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APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolisfe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
NUMBER OF SEQUENCES: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; DB 2; Length 24;
Pred. No. 1.85e+01;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           COUPTER: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,570
                                                                                                                                                                                                                                                                                                                    AUDRESSEE: Townsend and Townsend and Crew STRRET: One Market Plaza, Steuart Street Tower CIIY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 05 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 543-5600
TELEFAX: (415) 543-560
TELEFAX: (415) 543-5603
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acids
TYPE: ATTORNORY SES:
STANDEDDESS:
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                                                                                                             Sequence 127, Application US/08827570 Patent No. 5986047 GENERAL INFORMATION:
                                                                                 Sequence 127, Application US/08827570
                                                                                                                                                              APPLICANT: Wrighton, Nicholas C. APPLICANT: Dower, William J. APPLICANT: Chang, Ray S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 24 AA; 2547 MW; 2814 CN;
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ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 46.7%; 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: NIGHI HICKED STATES OF MORAXELLA
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
CARDESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
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Pred. No. 1.44e+01;
5; Mismatches 2; Indels
                                             Score 59; DB 2; Length 944;
Pred. No. 1.44e+01;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRENT STATICATION DATE

CLASSIFICATION NUMBER: US/08/867,941
FILING DATE: 03-JUN-1997
CLASSIFICATION: 435
ATTORNETINE: 435
ATTORNETINE STEWART INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 1038-681 MIS:jb
TELECOMUNICATION NUMBER: 1038-681 MIS:jb
TELECOMUNICATION NUMBER: 1038-681 MIS:jb
TELEPHONE: (416) 595-1153
TELEFAX: (416) 595-1153
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 944 amino acids
TYPE: amino acid
STANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                 944 AA.
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TOPOLOGY: linear
SEQUENCE 944 AA; 105523 MW; 4449713 CN;
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                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/08867941
Patent No. 5977337
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M
APPLICANT: Du, Run-Pan
                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/08867941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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Best Local Similarity 50.0%;
Matches 7; Conservative
                                             Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
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8 KSSKCVRQKVEGSS 21
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ID US-08-827-570-127
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US-08-867-941-24
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Best Local Similarity
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                                                                                           Sequence 127, Application US/08484631
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              Sequence 127, Application Patent No. 5830851
GENERAL INFORMATION: Wrighton, N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 543-504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   10 QGPKTWPCVRRRLGG 24
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APPLICANT:
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APPLICATION UMBER: US/08/484,635
FILING DATE: 07-UN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLOPEN PC COMPUTER: FLOREN PC COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/155,940 FILING DATE: 19-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
                                                                                                                                                                                                                                                      QGTKSSKCVRQKVEG
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CITY: S
STATE:
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ZIP: 941
                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               LE TYPE: peptide
24 AA; 2547 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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 Wrighton, Nicholas C. Dower, William J.
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Chang, Ray S.
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Jolliffe, Linda K.
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                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                  41.18;
46.78;
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                                                             US/08484631
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Best Local S
Matches
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                                                                                                                                       GENERAL
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APPLICANT:
APPLICANT:
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APPLICANT:
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STREET:
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TOPOLOGY: 11
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ZIP: 94105-1492
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Kashyap, Arun K.
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Sequence 2, Application US/08107042
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/155,940
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gairett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
                                                                                                                                                                                                    Sequence 2, Application US/08107042 Patent No. 5416014
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Local Similarity 46.78;
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INFORMATION FOR SEQ ID NO:
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                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                             APPLICANT: Burtscher, Helmut
APPLICANT: Schumacher, Gunther
TITLE OF INVENTION: CLONED N-CARBAMOYL
TITLE OF INVENTION: AMIDOHYDROLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
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                  ADDRESSEE: Armstrong, Nikaido, Marmelstein, ADDRESSEE: Murray
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
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24 AA; 2547 MW; 2814 CN;
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1725 K Street N.W., Suite 1000
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Mulcahy, Linda
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37,330
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/323,449
FILING DATE: October 14, 1994
APPLICATION NUMBER: U.S. 08/485,981
FILING DATE: June 7, 1995
ATTORNEY AGENT INFORMATION:
NAME: DOW, ALAN. E.
NAME: DOW, ALAN. E.
REGISTRATION NUMBER: 35,123
                 APPLICATION NUMBER: US/08/867,087B FILING DATE: June 2, 1997 CLASSIFICATION: 800
                                                                                                                                                  REFERENCE/DOCKET NUMBER: 4630-4707
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acid residues
TYPE: amino acid
        CURRENT APPLICATION DATA:
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Matches
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Patent No. 5990386
GENERAL INFORMATION:
APPLICANT: An, Gynheung
TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 1; Length 264; Pred. No. 3.90e+01; 4; Mismatches 3; Indels
                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,042
FILING DATE:
CLASSFICATION ADATA:
APPLICATION NUMBER: US/07/762,131
FILING DATE:
APPLICATION NUMBER: DE P 40 29 844.2
FILING DATE:
APPLICATION NUMBER: DE P 40 29 844.2
FILING DATE: 20-SEP-1990
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Ministon, LLP
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 212 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 AA.
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Washington D.C.
RY: United States of America
20006
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JENCE 264 AA; 29153 MW; 361847 CN;
                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 911286
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-659-2930
TELEFRAX: 202-887-0357
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MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                              NAME: Murray, Robert B. REGISTRATION NUMBER: 22,890
                                                                                                                                                                                                                                                                                                     TELEX: 440142
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 39.0%;
Best Local Similarity 46.2%;
Matches 6; Conservative
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US-08-867-087B-15
                     COUNTRY:
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Sequence 10, Application US/08353485
Patent No. 5830710
GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Lepine, Guylaine
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Corresph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEBE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
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COUNTRY: USA
ZIP: 34606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,485
FILING DATE: 09-DEC.1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/35,485
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/35,485
FILING APPLICATION A24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/35,485
FILING DATE: 25-JAN-1991
                                            Length 249;
                                                                          4; Indels
                                                                                                                                                                                                1732 AA.
                                           Match 38.3%; Score 54; DB 2; L. Local Similarity 26.3%; Pred. No. 4.99e+01; les 5; Conservative 10; Mismatches 4
                                                                                                                                                                                                PRT;
TOPOLOGY:, linear
WCE 249 AA; 28682 MW; 300604 CN;
                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08353485
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                                                                                                       160 EQMVSEANRCLRRKLEESN 178
                                                                                                                        3 DHQGTKSSKCVRQKVEGSS 21
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USA
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APPLICATION NUMBER:

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Best Local S
Matches
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MOLECULE TYPE: protein
SEQUENCE 1732 AA; 187874 MW; 16128552
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                                                                                                                                                                                                                                                                                                                                                XXXXX
                                                                              COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentID Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                Sequence 10,
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APPLICANT: Progul
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Local Similarity 31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (904) 372-58 INFORMATION FOR SEQ ID NO:
            FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 25-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                 2 IDHQGTKSSKCVRQKVEGS 20
                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 09-DEC-1994
                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                   APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis
TITLE OF INVENTION: and Probes for the Detection of
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1732 amino acids
                                                                                                                                                                                                                                       APPLICANT:
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TELECOMMUNICATION INFORMATION:
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CITY: 0
CLASSIFICATION: 424
NIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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5824791
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2421 N.W. 41st Street,
                                                                                                                                                                                                                                                      Tumwasorn, Somying
Lepine, Guylaine
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                        US 07/647,119
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Pred. No. 4.99e+01;
7; Mismatches 6; Indels
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: '1732 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 1732 AA; 187874 MW; 16128552 CN;
                                                   REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9990
TELEFAX: (212) 899-9741
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Shoyab, MC
APPLICANT: Plowman, G
TITLE OF INVENTION: P
TITLE OF INVENTION: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08431333
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CHASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 0'
APPLICATION NU
                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MISTORK, S. Lestie.
NAME: MISTORK, S. Lestie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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REGISTION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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: 589 amino acids amino acid
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Pred. No. 4.99e+01;
7; Mismatches 6;
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Best Local Similarity
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US-07-668-648-6
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GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321

FILING DATE: 19910403

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928

REFERENCE/DOCKET NUMBER: 32,928

REFERENCE/DOCKET NUMBER: 32,928

REFERENCE/DOCKET NUMBER: 32,928

TELEPHONE: (206)728-4800

TELEPHAION INFORMATION:
TELEPHAION INFORMATION:
TELEPHAIC (206)748-4775

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 389 anino acids
TYPE: AMINO ACID
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                                             Length 589;
                                           Score 53; DB 2; Length 589;
Pred. No. 6.38e+01;
7; Mismatches 2; Indels
                                                                                                                                                             589 AA
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3005 First Avenue
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MOLECULE TYPE: protein
JENCE 589 AA; 63501 MW; 1690383 CN;
         E TYPE: protein
589 AA; 63501 MW; 1690383 CN;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                             STANDARD;
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llarity 35.7%;
Conservative
                                           Query Match
Best Local Similarity 35.7%;
Matches 5; Conservative
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CITY: Seattle
STATE: Washington
COUNTRY: USA
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TOPOLOGY: linear
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PCT-US91-02321-6
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ID US-08-429-998-6
         MOLECULE
SEQUENCE 58
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Sequence 6, Application US/08429998

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Patent No. 5885961

CENERAL INTERPRATION: CRESCYL

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REFERENCE/DOCKET NUMBER: 5624
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                   XXXXXX
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                                                                                                                                                                                                                                                                                                                                                        PCT-US95-07754A-6
                                                                                                                                                                                                       Sequence 6, Application PC/TUS9507754A
GENERAL INFORMATION:
APPLICANT: Baker, Barbara J
APPLICANT: Whitham, Steven A
TITLE OF INVENTION: Plant Virus Resistance Gene and Methods
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                          560 HCSARGTKCLRKKI 573
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les 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                     4 HQGTKSSKCVRQKV
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ADDRESSEE: Margaret A. Connor, USDA-ARS
STREET: 800 Buchanan Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
           ATTORNEY/AGENT INFORMATION:
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                                                                                                                          COUNTRY:
ZIP: 947
                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                 CITY:
STATE:
                                 APPLICATION NUMBER: FILING DATE:
                      CLASSIFICATION:
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ZIP: 10036
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STATE: New York
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Connor, Margaret A
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                               TELEFAX: (510) 559-5777
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 DHQGTKSSKCVRQKVE 18
                                       TOPOLOGY: 110
MOLECULE TYPE:
JUENCE 652 AA;
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                     REFERENCE/DOCKET NUMBER: 00 TELECOMMUNICATION INFORMATION:
                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Connor, Margaret A
REGISTRATION NUMBER: 300
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Margaret A. Conn.
STREET: 800 Buchanan Street
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baker, Barbara J
APPLICANT: Whitham, Steven A
TITLE OF INVENTION: Plant Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 1: MOLECULE TYPE:
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LENGTH: 652 amino acids
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REFERENCE/DOCKET NUMBER: 000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 559-6067
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                        TYPE:
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STATE: CA
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Score 53; DB 1; I
Pred. No. 6.38e+01;
5; Mismatches 6
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Pred. No. 6.38e+01
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Search completed: Wed Sep 6 08:17:55 2000 Job time: 9 secs.

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Title:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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## SUMMARIES

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AR003797 AR010133 AR055339 I11980 AF1550 AF152308 AXU49832 AR027053 I110362 E10362 E10362 SYNN198SCF I45604 MM25478 A63778 A63778 A63778 A63776	ID A18692
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Db 184 CAGGGAAAATCTCCTGGTCTATGCTGCAACAAACTTAGCAGTGGTGTGCCA 243  184 TCTCGCTTCTGGATCCGGCTCCGGAACGGATTCACTCTGACCATCAGCAGTCTGCAG 243  18	QY 484 TGGGTGCGTCAGGCCCCGGGCCTGGAATGGATGGTGAGATCTTACCGGGCTCT 543	QY         544 GGTAGCACCGAATATACCGAAAATTTAAAGACCGTGTTACTATGACGCGTGACACTTCG         603	AR003797 723 bp DNA Sequence 89 from patent US 5744580. AR003797. G1:3965056 Unknown. Unknown. Unclassified. I (bases 1 to 723) Better, M.D., Carroll, S.F. and Studn Fumunotoxins comprising ribosome-in Patent: US 5744580-A 89 28-APR-1998	DASE COUNT 178 a 162 c 207 g 176 t  ORIGIN  OUETY MATCH  Best Local Similarity 63.7%; Pred. No. 5.3e-71;  Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps  OY 7 GATATCCAGATGACCCGTCCTCCTTCTGTGGGGGATAGGGTCACC 66
25         232.4         31.1         2178         5         AR048108         AR054190         Sequence           26         232.4         31.1         2178         5         AR054190         Sequence           27         232.2         31.1         2178         5         AR060673         AR060673         AR060677         AR060677         Sequence           29         230.6         30.9         1220         5         AR060676         AR060674         Sequence           30         230.6         30.9         1320         5         AR060676         AR060674         Sequence           31         230.6         30.9         1320         5         AR060676         AR060674         Sequence           32         230.6         30.9         6799         AR060676         Sequence           32         22.5         30.1         790         12         MWAJ24FRG         AR060676         Sequence           33         224.8         30.1         819         5         AR02705         AR02705         Sequence           34         224.4         30.0         732         AR02705         AR02705         Sequence           37         224.4	ALIGNMENTS	RESULT 1 A18692 LOCUS B19 bp DNA PAT 06-JUL-1995 LOCUS DEFINITION Synthetic nucleotide B72.3 single chain FV hinge. ACCESSION A18692 VERSION A18692.1 GI:513358 KEYWORDS ONCE Synthetic construct. ORGANISM Synthetic construct artificial sequence. REPERENCE (bases 1 to 819)	TATLE  AUGUNAL  Patent: WO 9119739-A 26 26-DEC-1991;  FEATURE  Location/Qualifiers  Location=State=1  / Absentance=1	TN Match st Local Similarit tches 439; Conse 4 GCGATATCAG 1   1   1   1   1   1   1   1   1   1

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ATGCCGCGCTGAACTGGTATCAACGTAAACCT 126
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GGATTTCACTCTGACCATCAGCAGTCTGCAG 243
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Better,M.D., Carroll,S.F. and Studnicka,G.M.
Immunotoxins comprising ribosome-inactivating
Patent: US 5756699-A 89 26-MAY-1998;
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Sequence 89
AR055339
AR055339.1
                                                1 (bases 1 to 723)
Better, M.D., Carroll, S.F. and Studnicka, G.1
Polynucleotides encoding gelonin sequences
Patent: US 5837491-A 89 17-NOV-1998;
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Unclassified
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Query Match 37.18 Best Local Similarity 63.78 Matches 472; Conservative

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Score 283.4; DB 5; Pred. No. 5.3e-71; 0; Mismatches 251;

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GATATCCAGATGACCCAGTCCCGGTCCTGTCGCGCGTAGGGTCACC	SACATCCAGATGACTCAGTCTCCATCTTCCTGCATCTGTAGGAGACAGAGTCTCTGTAGGAGACAGAGTCACCTGCCTG		GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGAACCTGGCAGATGGAGTCCCTTCT	GGGAAAGCTCCTAAGACCCTGATCTATCGTGCAAAAGAGTTGGAATCTGGGGTCCCATCA CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCT		GAAGACTICGCTACGIATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG	GAAGATTTTGGAATTTATTGTCAACAGTATGATGAGTCTCCGTGGACGTTCGGTGGA	GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTTCTGGTGGCGGGGGGTGGATCTGGT 	GGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCC	SGTGGAGGATCTGAGATCCAGTTGGTGCAGTCTGGAGGGGGGGCCTGGTGAAGCCTGG TCAGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTTT		GTGCGTCAGGCCCCCGGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGT 	AGCACCGAATATACCGAAAATTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACT	GAGCCAACATATGCTGATTCTTTCAAGGGACGGTTTACCTTCTTTGGACGATTCTAAG	AGTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGC	SCGCGTTATTTTTGGTTCTAGCCCGAATTGGTATTTGATGTTTGGGGTCAAGG	ACAAGACGGGGTTACGACTGGTACTTCGATGTCTGGGGCCAAGGGACC	CIGGICACIGICAGCIGA 747		I11980 723 bp DNA PAT 26 Sequence 92 from Patent US 5416202. I11980 I11980.1 GI:909423	Unknown. Unknown. Unklassified. 1 (Joses 1 to 723) Bernhard,S.L., Better,M.D., Carroll,S.F., Lane,J.A. and Materials comprising and methods of preparation and use ribosome-inactivating proteins Patent: US 5416202-A 92 16-MAY-1995; Location/Qualifiers
~	1 67	61	127	121	181	247	241	307	367	427	415	487	547	535	595	667	655	727	<u> </u>	RESULT 5 111980 LOCUS DEFINITION ACCESSION VERSION	REYWORDS SOURCE SOURCE REFERENCE AUTHORS TITLE JOURNAL FEATURES

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CTTCCCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
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Pred. No. 5.3e-71;
0; Mismatches 251; Indels 18;
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                  GCAGATGGAGTCCCTTCTCGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACC
                                                                               TGGTATCAACGTAAACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTG
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ANATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC
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2 (bases 1 to 888)
Doyen.C., Alcocer,M.J.C., Lee,H.A. and Morgan Direct Submission 99) Biochemistry, Institu Submitted (01-MAR-1999) Biochemistry, Norwich,
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TLTISSYKAEDLAVYYCHQYYRYPTFGSGTKLEIKGGGSGGGGGGGGGGGG
KULKKOSGPELARPGASYKCHQYRYFYFRYWAYWKQRYGGGEMIGAIYPGHQDTK
YQLKQSGPELARPGASYKLGCKASGTFHRYWAYWYCYFYYGSDDYVMDYWGQGTSVT
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/db_xref="GI:4928297"
/translation="MKYLLPTAAAGLLLLAAQPAMADYKDIVMTQSPSSLAVSVGEKV
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/transl_table=11
/product="anti-chlorpyrifos-ethyl scFv recombinant
immunoglobulin"
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/note="Mus musculus, strain
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/db_xref="taxon:32630"
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No. 8e-65;
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/transl_table=11
/product="single chain Fv antibody"
/protein_id="AAA92722.1"
/db_xref="GI:1236091"
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OGKSPQLLVYSAKTLAEGVPSRFSGSGSGTQFSLKINSLQPEDFGSYYCQHHYDTPRT
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1 (bases 1 to 902)

Chen,2.C., Cockburn,W., Torrance,L., Barker,H. and Whitelam,G.C.
Cytoplasmic accumulation of a soluble functional scry protein to a plant virus expressed as a thioredoxin fusion in Escherichia coli on bubblished
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Submitted (13-FBE-1996) Z.C. Chen, Botany, Univ. of Leicester, University Road, Leicester LEI 7RH, UK
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                                                           GGIGGIGCTICTGGIGGCGGIGGATCTGGIGGTGGCGGTTCTCAAGTCCAACTGGIGCAA 396
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antibody against potato virus V coa
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            TCCGGCGCCCGAGGTCAAGAAGCCAGGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGC
                                                                                                                                                      TGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGAC
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                                               CCGTTGACTTTCGGACAGGGTACCAAGGTGGAAATAAAAC----
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/organism="synthetic o/db_xref="taxon:32630"
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SYKMSCKASGYTFTSYNMHWYKQTPGQGLEWIGYIYPGNGTIYNOKFKGKATLTADT

SSSTANWQISSLISEDSAYYFCARGDYRNDPFDFWGQGTTLTVSSAKTTPPSVYPLAP

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                                                                                                                                                             Length 902;
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Sequence 3 from patent US 5856140.
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Best Local Similarity 61.4%;
Matches 482; Conservative (
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                                      GCAAGAGAGAATTACTACGGTAGTAGCTACGGG - - - TTTGCTTACTGGGGCCAAGGGACT
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complement C5 inhibitor; inclusion body protein.
Synthetic construct

artificial sequence.

E 1 (bases 1 to 780).
S Evans, M.J. Rollins.S.A., Wolff, D.A., Rother, R.P., Norin., A.J.,
Th, D.M., Mueller, J.P., Nye, S.H., Squinto, S.P. and Wilkins, J.A.
In vitro and in vivo inhibition of complement activity by a single-chain Fv fragment recognizing human C5

L MOI. Immunol. (1995) In press
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Synthetic single chain Fv (N19-8 scFv) DNA fragment.
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Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                      GCGCGTTATTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAACC 726
                                         Gaps
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C12N15/13//C12N15/06,
(C12P21/08,C12R1:19),(C12P21/08,C12R1:91),(C12N1/21,C12R1:19);
Key
                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding an monoclonal antibody against human Interleukin-2 receptor gamma chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimamura T., Hamuro J., Nakazawa H., Kanayama Y.,
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                                                                                                                                                                                                                                                                                                                                                         08-OCT-1997 (Rel. 52, Created)
08-OCT-1997 (Rel. 52, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .729
/organism="Mus sp."
/cell_type="hybridoma"
/cell_line="GP-4"
1. .729
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"IMMUNDUPRESSIVE AGENT";
Patent number JP 1995313188-A/2, 05-DEC-1995.
AJINOMOTO CO INC, SUGAMURA KAZUO,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"anti-IL-2
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21-APR-1993 UP 93P 944
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05-DEC-1995
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                             ACAGCCTTGTATTTCTGTGTAAGAGAGACTTATTACTACGGGATTAGTCCCGTCTTCGAT
                                             TCCAGAGACAATGCCAAGAGCACCCTGGATCTGCAAATGAGCAGTCTGAAGTCTGAGGAC
                                                                                                        ACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGAGGAC
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/protein_id="AAA68906.1"
/db_xref="GI:870722"
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                                        CCGGGCTCTGGTAGCACCGAATATATCGACGAAAATTTTAAAGACCGTGTTACTATGACGCGT
                                                                                            TCTGGTGGTGGCGGTTCTC-----AAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAG 414
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                          CCATACAAAGGTCTTACTACCTACAACCAGAAATTCAAGGGCCAAGGCCACATTAACTGTA
                                                                               ATCGTGAACTGGCTGAAGCAGAGCCATGGAAAGAACCTTGAGTGGATTGGACTTATTAAT
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Ledbetter, J.A., Gilliland, L.K., Hayden,
Bajorath, J. and Fell, H. Perry,
Expression vectors encoding bispecific
of producing biologically active bispec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent: US 5637481-A 29 10-JUN-1997;
Location/Qualifiers
1. .916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mammalian cell
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223 c 228 g
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Pred. No. 1.5
0; Mismatches
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Mismatches 288
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----ATGGCGCGCTGAACTGG

231 258 291 318 351 372 411 432

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79 ATCTCTTGCAGATCTAGTCAGAGCATTGTACATAGTAAAGGAAACACCTATTTAGAATGG 138
                                                                                             112 TATCAACGTAAACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCA 171
 19 GACATCCAGATGACACAGTCTCCACCCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCC 78
                                                                                                                                                                                                                                                                                                              232 AGCAGICIGCAGCCIGAAGACTICGCIACGIATIACIGICAGAACGITITAAATACICCG
                                                                                                                                                                                                                                               292 TTGACTTTCGGACAGGGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTGGT
                                                                                                                                                                                                                                                                                                                                                           352 GGCGGTGGATCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTC
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/product = 1gg3/kappa antibody"
/product = 1gg3/kappa antibody"
/protein_id="Cap08856_1"
/db_xref="G1:2108313"
/db_xref="G1:2108313"
/db_xref="G1:XNSDESQNDSPPSLPVSLGDQASISCRSSQSIVHSKGNTYL
FWRLQKPGOSPKLLIYKVSNRPSGVPDRFSGSGSGSTDFTLKISRLEAEDLGVYYCFQG
SHVPYTFGGGTKLEIKGGGGGGGGGGGSEVQLQESGAELVRSGASVKLSCTASDF
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LTSEDTAVYYCNAYGNYDGYRGQGTTVTVSSAKTTVGAAAEQKLISEEDLNDIKDEL"
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/note="Light chain variable domain (V1) coding sequence"
355. 399
/note="Linker peptide coding sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Heavy chain variable domain (Vh) coding sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (07-MAY-1997) Dept. of Nematology, Wageningen
Agricultural University, P.O. Box 8123, Wageningen 6700 ES, The
Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chases I to 828)
Schouten, A., Roosien, J., de Boer, J.M., Wilmink, A., Rosso, M.N.,
Bosch, D., Stiekema, W.J., Gommers, F.J., Bakker, J. and Schots, A.
Improving Screv antibody expression levels in the plant cytosol
FEBS Lett. 415 (2), 235-241 (1997)
Gaps
                                                                                                                                                                                                                           MMZ95478 828 bp mRNA ROD 29-OCT-1997
Mus muscullus mRNA for IgG3/Kappa antibody, scFv49-CK.
295478 AF004405
295478.1 GI:2108312
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 828)
Schouten, A.
                                              GTCTATTATTGCGCGCGTTATTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 828;
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Pred. No. 4.3e-60;
0; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="c-myc tag coding sequence"
814. .825
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196 c 228 g 186 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/note="recombinant gene"
                                                                                                                                 Location/Qualifiers
                                                                                                           715 GGTCAAGGAACCCTGGTCACTGTCTC 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coding sequence"
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62.9%;
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Best Local Similarity 62.9
Matches 424; Conservative
                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                            house mouse.
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MEDLINE
FEATURES
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AUTHORS
TITLE
JOURNAL
                                                                                                                                           793
                                                                                                                                                                                                                                                          ACCESSION
VERSION
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AUTHORS
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531

591 612 651

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12-MAR-1998
                                                                                                                                                 1 (bases 1 to 1149)
Bebbington.C.R., Lawson,A.D., Weir,A.N. and Finney,H.M. CELL ACTIVATION PROCESS AND REAGENTS THEREFOR PATENT: WO 9723613-A 42 03-UTL-1997;
CELLTECH THERAPEUTICS LTD (GB)
Other publication AU 1201997 19970717.
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 239.6; DB 5; Length 1149; Pred. No. 2.3e-58;
       PAT
                                                                                                                                                                                                                                                                                                                                        267
         DNA
WO9723613.
                                                                                                                                                                                                                                                                                                  /organism="unidentified"
/db_xref="taxon:32644"
1 288 c 309 g 267
                                                                                                                                                                                                                                                                 Location/Qualifiers
A03/78 1149 bp
Sequence 42 from Patent
A63778
                                                                                                                                                                                                                                                                                                                                                                                                                 32.1%;
62.0%;
                                                           A63778.1 GI:3717351
                                                                                             unidentified
unidentified
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Best Local Similarity
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7 GATAICCAGAIGACCCCGTCCTCCCTGTCCGCCTCTGTGGGCGAIAGGGTCACC 66

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                                                                                                                         540 TIGTAAGGCATCTGGATACACCTTCACCGACTACTACATTAATTGGATGAGACAGGCACC
                                                                                                                                      441 CTGTAAAGCTAGCGGCTATATTTTTTTCTAATTGATTGGATTCAATGGGTGCGTCAGGCCCC 500
                                                                                                                                                                 240 CAGTGGTGTACCATCTAGATTCAGTGGTAGTGGTAGTGGTACTGAGTTCACTCTCACTAT
                                                                                                                                                                                                                                                                                                                                               171 AGATGGAGTCCCTTCTCGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCAT 230
                                                                                                                                                                                                                                                                                                                                                                                180
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           GGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGCGC 668
                                                   CGAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACAT 620
                                                                                              CGGGCAGGGCCTGGAATGGATGGGTAGATCTTACCGGGCTCTGGTAGCACCGAATATAC 560
                                         TGAGAAGTTCAAGGGAAGAGCAACACTGACAGTGGACACATCCACGAATACCGCCTACAT 719
                                                                                TGGACAGGGACTCGAGTGGATTGGATGGATTGACCCTGGATCTGGAAATACAAAGTACAA 659
                                                                                                                                                                                                                                                                                                                                                                            CGATATCCAGATGACCCAGTCCCCGTCCTCCCTGTCGCCTCTGTGGGCGATAGGGTCAC 65
GGAGCTGTCTCTGAGATCTGAGGACACAGCATTCTACTTCTGTGC 767
                                                                                                                                                                                                                                                                                                                                                                                                                                          CATCACCTGCGGCGCCAGCGAAAACATCT------ATGGCGCGCGCTGAACTG 110
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Search completed: September 12, 2000, 20:36:42 Job time: 4618 sec

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Title:
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121: gb_gss17:*
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123: gb_gss18:*
124: em_gss13:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	07904 UI-HF	05753 UI-HF-	05301 UI-HF-	AW406294 01-HF-BL0	00001 01-BF-BD	4714 OI HF BD	05752 UI-HF-BL	05906 UI-HF-BL	91263 QVO-ST02	04992 UI-HF-	83563 PM4-HT	591 UI-	05900 UI-HE-	06828 UI-HF-	01347 EST142	4507 UI-HE-	06939 UI-HF-	05761 UI-HF-BL	05241 UI-HF-BL	04458 UI-HF-BL	4748 UI-HF-BL	04099 UI-HF-BL	03686 UI-HF-BK	06562 UI-HF-BL	03684 UI-HF-	06228 UI-HF-BL	4894 UI-HF-BL	SAS ESTIUDESS	JAROP OI-HE-	3.4.5 UI - HF - BL	12-3H-111 12-3L	2603 III - HE-BK	05988 UT-HF-BI	08270 UT-HF-BK	1363 oh68a09.	162845 HS 5207	6227 UI-HF-BL	30201 xf29h0	02294 UI-HF-	02942 UI-HF-	7113 UI-HF-	623 UI-HF-	04145 UI-HF-
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ALIGNMENTS

AW407904 422 bp mRNA EST 16-FEB-2000 UI-HF-BL0-add-a-01-0-UI.r2 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061128 5', mRNA sequence.

RESULT 1
AW407904
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DEFINITION

RESULT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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1 National Institutes of Health, Mammalian Gene Collection (MGC)

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/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2:5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

110 c 105 g 101 t ö 187 CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT 246 262 Gaps ATCACCTGCGCCCCAGCGAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126 GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT 186 GAAGACTICGCIACGIATIACTGTCAGAACGITTIAAAIACTCCGTTGACTTTCGGACAG 306 23 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGTAGGAGACAGAGACACCC 82 7 GATATCCAGATGACCCAGTCCCCGTCCTCTCTCCCCTCTGTGGGCGATAGGGTCACC 66 203 AGGTICAGIGGCAGIGGAICTGGGACAGAITICACTCTCACCATCAGCAGTCTGCAACCT ; 0 Query Match 26.0%; Score 194.2; DB 72; Length 422; Best Local Similarity 72.9%; Pred. No. 1.8e-49; Matches 250; Conservative 0; Mismatches 93; Indels 0; /clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85" /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:3061128" Location/Qualifiers AW407904 AW407904.1 GI:6926961 106 source BASE COUNT ORIGIN ORGANISM AUTHORS TITLE JOURNAL COMMENT 29 83 127 247 307 323 ACCESSION VERSION KEYWORDS SOURCE REFERENCE FEATURES 셤 g 셤 à ŏ 셤 ŏ g à ò å

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                                                                                                                                       GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCGGACGTTCGGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian
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Seq primer: M13 Forward.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/clone="IMAGE:3057290"
/clone_lib="NIH_MGC_37"
/tissue_type="1ymph"
/cell_type="germinal center B content of the content of 
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/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_1: 
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Pred. No. 5.7e-48;
0; Mismatches 96;
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                                                                                    CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT
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UI-HF-BLO-ack-b-02-0-UI.rl NIH_MGC_37
IMAGE:3059259 5', mRNA sequence
AW405301
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MCC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Onpublished (1999)
On Jul 8, 1999 this sequence version replaced gi:5421949
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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National Institutes of Health, Mammalian
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1 (bases 1 to 487)
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/constructed from size fractionated cytoplasmic mRNA
(1.5-2.5b). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

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/cell_line="MGC85"
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/db_xref="taxon:9606"
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/note="Vector: pT773-pac; Site_l: NotI; Site_2: Eco RI;
/note: pT773-pac; Site_l: NotI; Site
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1 (bases 1 to 471)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

On May 11, 1999 this sequence version replaced gi:4776604.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausberg(anh.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CLONA Library Arrayed by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

www-bio.llnl.gov/bbrp/image/image.html

Seg primer: M13 Forward.
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   282 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTGCCCCGTACAGTTTTGGCCAG 341
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                                                                                                                                                                                                                                                                                              AW406294 471 bp mRNA EST 16-FEB-2000 UI-HF-BLO-aco-b-09-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059657 5', mRNA sequence.
AW406294 GI:6925351
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Pred. No. 1.7e-46;
0; Mismatches 99; Indels
                                                                307 GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTTCTG 349
                                                                                                  Location/Qualifiers
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Best Local Similarity 71.1%;
Matches 244; Conservative (
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/clone_lib="MIH_MGC_37"
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/
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On May 11, 1999 this sequence version replaced gi:4776388.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg(hih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
CONA Library Arrayed by: M.B. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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NIH-WGC http://www.nobi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                          297 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCGTGGACGTTCGGCCAA 356
237 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 296
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                                                                                                        GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG
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AW406081.1 GI:6925102
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BASE COUNT
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Best Local S
Matches 242
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                                                                                                                                             Local Similarity
les 242; Conserv
ACCTGCGGCGCCAGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCTGGG
                                                            CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT
                                                                                                      ATCCAGATGACCCAGTCCCCGTCCTCTGTCCGCCTCTGTGGGCGATAGGGTCACCATC 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGATTTTGCAGCTTACTACTGTCAACAGAGTTACACTACCCCGCTCACTTTCGGCGGA 364
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AW404714 608 bp mRNA sequence.
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National Institutes of Health, Mammalian
Unpublished (1999)
On Jan 6, 2000 this sequence version repl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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1 (bases 1 to 608)
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                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                /lab_host="DHIOB (LTI)"
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(1.5-2.5kb). Directionally cloned. Cells provided by Lou
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
169 c 146 g 135 t
                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:3058580"
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/cell_type="germinal center B
/cell_line="MGC85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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71.2%;
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                                                                                                                                         Score 183.2; DB 72;
Pred. No. 5e-46;
D; Mismatches 98;
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                      129
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Best Local S
Matches 243
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GATATCCAGATGACCCAGTCCCCGTCCCTGTCCGCCTCTGTGGGGGGATAGGGTCACC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATTTTGCAACTTACTTCTGTCAGCAGAGTTTCACCTACCCCGTACAGTTTTGGCCAGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAA
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Jan 6, 2000 this sequence version replaced g1:6675906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.National Institutes of Health, Mammalian
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1 (bases 1 to 431)
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IMAGE:3061499
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                                                                               Similarity
                                                                                                                                                                                      101
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                                                                                                                                                                            'llab_host="DHIOB (LTI)"
'note="Yector: pT/T3-Pac; Site_1: Not1; Site_2: Eco RI;
'note="Yector: pT/T3-Pac; Site_1: Not1; Site_2: Eco RI;
'Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

125 c 105 g 100 t
                                                                                                                                                                                                                                                                                                          /tissue_type="lymph"
/cell_type="germinal center B
/cell_type="MGC85"
/lab_host="runca5"
                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3061499"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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                                                                               24.5%;
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-h-06-0-UI.rl NIH_MGC_37
5', mRNA sequence.
                                                          Score 183; DB 72;
Pred. No. 5.2e-46;
0; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens cDNA clone
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                                                                                                Length 431;
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AW405906.1 GI:6924963
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  Matches 243; Conservative
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KEYWORDS
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E. (bases 1 to 447)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Onpublished (1999)

On Aug 21, 1998 this sequence version replaced gi:3707751.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergen, Ph.D.

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CONA Library Preparation: M.B. Soares Lab

CONA Library Arrayed by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINE at:

www-bio.lnl.gov/bbrp/image/image.html

Seq primer: Mil Forward.
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/cell_tipe="germinal center B cells"
/cell_type="germinal center B cells"
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/note="vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;
/constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                 246
                                                                                                                                                              240 AGGITCAGIGGCAGIGGAICIGGGACAGAIIICACICICACCAICAGCAGCAGCAGCAGCAACCI 299
  60 GACATCCAGATGACCCCAGTCTCCATCCTCCTGTTCGCATCTGTAGGAGACAGAGTCACC 119
                                                                                           ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTTTTTAAATTGGTATCAGCAGAAACCA 179
                                                                                                                                                                                                                                                                                                                         GAAGACTICGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTIGACTTTCGGACAG 306
                                                                                                                                                                                                                                                                                                                                                                    GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACACTACCCCTCGCACTTTCGGGGGA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UI-HF-BLO-abp-a-01-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3057288 5', mRNA sequence.
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                                             ATCACCTGCGCCCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT
                                                                                                                                                                                                                              187 CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            307 GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTG 349
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Pred. No. 5.3e-46;
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/organism="Homo sapiens"
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/clone="IMAGE:3057288"
/clone_lib="NH_MGC_37"
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70.8%;
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Best Local Similarity
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE JOURNAL

COMMENT

FEATURES

REFERENCE

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RESULT AW405752 LOCUS

BASE COUNT ORIGIN

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Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi;
Eukaryota: Metazoa: Chordata: Catarrhini; Hominidae: Homo.

El (Dases I to 460)

I (Dases I to 460)

IN IH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

In Dupublished (1999)

In Jul 8, 1999 this sequence version replaced gi:5422554.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Emmil: Robert_Strausberg@nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CLONA Library Arrayed by: M.B. Soares Lab

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/Dbrp/image/image.html

Seq primer: MN3 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                  246
                                                                                                                                                                                                 203 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAGAGTGGGGTCCCATCA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 GAAGATTTTGCAACTTACTACTGTCAACAGAGCTACGAGTACCCCGTACCAGTTTTGGCCAG 382
                                                                                                                                                                   ATCACCTGCGGCGCCAGCGAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
                                                                                                           83 GACATCCAGATGACCCAGICTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW405906 460 bp mRNA EST 16-FEB-2000 UI-HF-BL0-acg-a-12-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058847 5', mRNA sequence.
                                                     99
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                263 ACGITCAGIGGCAGIGGAICTGGGACAGAITTCACTCTCACCAICAGCAGTCTGCAACCI
                                                     7 GATATCCAGATGACCCAGTCCCCGTCTGTGCCCCTCTGTGGGCGATAGGGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                  187 CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT
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RESULT 10
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                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=QV0&t2=QV0-ST0214-
291199-064-d06&t3_1999-11-29&t4-1)
                                                                                                                                                                                                                                                                                                                                                                                         The FAPESP/LICE Human Cancer Genome Project Unpublished (199)
On May 18, 1998 this sequence version rooter.
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QVO-ST0214-291199-064-d06 ST
AW391263
                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note-"Organ: stomach; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application NO. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                            /clone_lib="ST0214"
/dev_stage="Adult"
                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
On May 20, 1999 this sequence version replaced Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                     Eco RI site shown at the beginning of the sequence Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/Dbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                             Robert_Strausberg@nih.gov
/organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3058060"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B
/cell_line="MGC85"
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            /note="Vector: pT/T3-Pac; Site_1: Not1; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (15-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-HT0348-26199-001-A97&t3=1999-11-26&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 452.
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PM4-HT0348-261199-001-A07 HT0348 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                            187 CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT 246
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HCGP http://www.ludwig.org.br/ORESTES.
HCGP https://ICR Human Cancer Genome Project
Unpublished (1999)
On Jan 6, 2000 this sequence version replaced gi:6672417.
                                                                                                                                                                                   ;
0
                                                                                                                                                      Length 391;
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                                                                                                                                                   Score 179.8; DB 72;
Pred. No. 5e-45;
0; Mismatches 92;
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/lab_host="DH10B (LTI)"
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milarity 71.9%; 1
Conservative 0;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammanlai Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 488)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Lontact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

ECO RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
/clone_lib="HT0348"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_l: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
a 125 c 107 g 113 t
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Pred. No. 5.2e-45;
0; Mismatches 102;
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Seq primer: M13 Forward.
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Best Local Similarity 70.3%;
Matches 241; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGCCCACTCCCAGGTCCAGCTTGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCT 107
                Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
                                                                                        Unpublished (1999)
on May 11, 1999 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                               AW405900 426 bp mRNA
UI-HF-BLO-acg-a-03-0-UI.rl NIH_MGC_37
IMAGE::3058829 5', mRNA sequence.
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AW405900.1 GI:6924957
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cDNA Library Arrayed by: M.B. Soares Lab
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/clone="IMAGE:3056184"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B c
/cell_line="MGC85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B (LTI)"
/note="Vector: pTT3: Site_1: Not1; Site_2: Eco RI;
/note="Vector: pTT3: Site_1: Not1; Site_2: Eco RI;
Constructed from s1ze fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
a 136 c 140 g 101 t
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                                                                                                                                                                                                                                                                  UI-HF-BLO-adg-a-09-0-UI.rl NIH_MGC_37 Homo IMAGE:3061169 5', mRNA sequence.
AW406828
                 Unpublished (1999)
on Jan 6, 2000 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                        Mammalia; Eutheria; Primates; Catarrhini
1 (bases 1 to 466)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: M.B. Soares Lab
Clone distribution: MCC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                               human.
                                                                                                                                                                                                                                                  AW406828.1 GI:6925885
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/db_xref="taxon:9606"
/clone="IMAGE:3058829"
/clone=lib="NIH_MGC_37"
/tissue_type="lymph"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B (LTI)"
/note="Vector: pT7T3-Pac;
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/cell_line="MGC85"
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Pred. No. 5e-44;
D; Mismatches 104;
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                                                       replaced
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Cocation/Qualifiers

1. 466
/ Organism="know sapiens"
/ Organism="know sapiens"
/ Ab_xref="taxon:9660"
/ Clone="InAGE:3061169"
/ Clone="lib="NIH_MGC_37"
/ tissue_type="lymph"
/ cell_type="lymph"
/ cell_line="MGCB5"
/ lab_host="ablue (LTI)"
/ lab_host="ablue (LTI)"
/ note="vector: p777-Pac; Site_1: NotI: Site_2: Eco RI;
/ note="vector: p777-Pac; Site_1: P77
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Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnl.gov/bbry/image/image.html

Seq primer: M13 Forward.
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ORIGIN
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Search completed: September 12, 2000, 20:04:48 Job time: 3485 sec

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Total number of hits satisfying chosen parameters:
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Best Local Similarity 100.0%;
Matches 747; Conservative (
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Evans MJ, Matis L, Mueller E.
Rother RP, Springhorn J P, S
Wang Y, Wilkins JA;
WPI: 95-39293/50.
P-PSDB; R77607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating glomerulonephritis with antibody against complement C5 component to inhibit complement induced cell lysis Claim 33, Page 110-113; 181pp; English.

NNA (T08480) coding for humanised CDR-grafted scFv CB (R77607) was derived from DNA of hybridoma ATCC HB 11625, the producer of anti-C5 monoclonal antibody (MAb) 5G1.1. The DNA was subcloned into vector pET Trc SO5/NI for expression in Escherichia coll. The 119ht and/or heavy chain CDRs of scFv CB can be combined with CDRs from other 5G1.1-derived antibodies, Fds and light chains (R77607-16) in the produ. of recombinant, including humanised, antibodies that retain the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           708480;
15-MAR-1996 (first entry)
15-MAR-1996 (first entry)
Humanised CDR-grafted 5G1.1 scFv CB DNA.
Complement C5; haemolysis; kidney; glomerulonephritis;
monoclonal antibody; antiinflammatory; antiibody engines
humanised antibody; complementarity determining region
single chain antibody; scFv; ds.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                       associated with glomerulonephritis. Sequence 747 BP; 161 A; 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-1995.
01-MAY-1995; U05688.
02-MAY-1994; US-236208.
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  CCTTCTCGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTG
                                         AAACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTC
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V63620
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V63840
T91614
T35691
T86646
Q73678
X07474
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Squinto SP,
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Pred. No. 5.7e-199;
; Mismatches 0;
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region; CDR;
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                                                                              Treating glomerulonephritis with antibody against complement C5 component to inhibit complement induced cell lysis claim 34; Page 138-140; 181pp; English.

A DNA construct (T08480) codes for a humanised CDR-grafted scrv, designated 5G1.1 scFv DO12 (R77616), which includes CDRs derived from mouse anti-c5 monoclonal antibody 5G1.1. The DNA can be subcloned into vector pET Trc SO5/N1 (see T08489) for expression of humanised scFv in Escherichia coll ME1 cells. Such recombinant antibodies retain the ability of MAD 5G1.1 to block
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                              CAGCCTGAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTC
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T08488;
15-MAR-1996 (first entry)
Humanised CDR-grafted 5G1.1 scFv DO12 DNA.
COmplement C5; haemolysis; kidney; glomerulonephritis;
monoclonal antibody; antiinflammatory; antibody engineering;
humanised antibody; complementarity determining region; CDR;
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Squinto SP,
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02-MAY-1995; U05688.
02-MAY-1994; US-236208.
(ALEX-) ALEXION PHARM INC.
EVANS MJ, MAILS L, Mueller EE
Rother RP, Springhorn J P, Sq
WMI Y, Wilkins JA;
WPI: 95-392923/50.
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Murine 5G1.1M1 scFv DNA.
Complement C5; haemolysis; kidney; glomerulonephritis;
monoclonal antibody; antiinflammatory; antibody engineering;
humanised antibody; complementarity determining region; CDR;
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                                                                                                                              Indels
human complement C5a generation and thus to reduce inflammation and kidney dysfunction associated with glomerulonephritis.
Sequence 747 BP; 159 A; 190 C; 210 G;
                                                                                             Score 729.4; DB 1
Pred. No. 4.5e-194
0; Mismatches 11
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98.5%;
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T08479;
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Best Local Similarity 98.5
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DNA (T08479) coding for murine scFv 5G1.1M1 (R77606) was obtd. by PCR cloning of DNA from hybridoma ATCC HB 11625, the producer of anti-C5 monoclonal antibody (MAD) 5G1.1. The DNA was subcloned into pET Trc S05/NI for expression in Escherichia coll. The light and/or heavy chain CDRs of scFv 5G1.1M1 can be combined with CDRs from other 5G1.1-derived antibodies, Fds and light chains (R77607-16) in the produ. of recombinant, including humanised, antibodies that retain the ability of MAD 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated with glomerulonephritis.
Sequence 747 BP; 183 A; 174 C;
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                                                                                                          GGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTCTAATTATTGGATT
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AGTGGTTCTACTGAGTACACTGAGAACTTCAAGGACAAGGCCGCATTCACTGCAGATACA
                                                          GGGCCTCAGTGAAGATGTCCTGCAAGGCTACTGGCTACATATTCAGTAACTACTGGATA
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-1994; US-236208.
) ALEXION PHARM II
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Pred. No. 2e-101;
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                                                                                                                                                                                                                                                                                                                                                                                                        Treating glomerulonephritis with antibody against complement C5 component - to inhibit complement induced cell lysis Claim 38; Page 123-125; 181pp; English.

A DNA construct (708483) codes for a humanised CDR-grafted and framework sequence-altered Fd 5G1.1 VH + IGHRL (R77610), which includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.

The DNA can be subcloned together with DNA (708484) coding for a humanised light chain (R77612) into vector APEX-3P (708476) for expression of humanised antibody in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with Sequence 750 BP; 163 A; 220 C; 197 G; 170 T;
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Best Loc
Matches
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01-MAY-1995; U05688.
02-MAY-1994; US-236208.
(ALEX-) ALEXION PHARM INC.
EVANS MJ, MATIS L, Muelle
Evans MJ, Matis L, Muelle
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Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complement C5; haemolysis; kidney; glomerulonephritis; monoclonal antibody; antiinflammatory; antibody engineering; humanised antibody; complementarity determining region; CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-APR-1996 (f)
Humanised 5G1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          signal_peptide
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                                                                                              97
                                                                                                                                                                                                37
                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                            Match
                                                                                         GGATCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCCGAGGTCAAGAAG
                           GTAACTGCCGGCGTCCACTCCCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGACCACGGTCACCGTCTCCTCATGA
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al Similarity
377; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b
58. .747
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1. .57
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                                                                                                                                                                                                                                                                                                              49.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                          Score 371; DB Pred. No. 2.7e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA.
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Squinto SP,
                                                                                                                                                                                                                                                                                                                DB 1;
.7e-94;
                                                                                                                                                                                                                                                                                            Indels
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216
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mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 GGATCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCCGAGGTCAAGAAG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating glomerulonephritis with antibody against complement C5 component - to inhibit complement induced cell lysis (laim 37; Pages 135-137; 181pp; English.

A DNA construct (1708487) codes for a humanised CDR-grafted light chain, designated 5G1.1 VI + IGHRLD (R77615), which includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The DNA can be subcloned together with DNA (1708484) coding for a humanised FG (R77611) into vector APEX-3P (T00476) for expression of humanised antibody in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAD 5G1.1 to block
          GGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGAC
                                                   TATTATTGCGCGCGTTATTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGGT
                                                                                                     TATTATTGCGCGCGTTATTTTTTGGTTCTAGCCCCGAATTGGTATTTTGATGTTTGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glomerular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.0%; Score 358.2; DB 1; Length 750; 95.3%; Pred. No. 9.8e-91; ive 0; Mismatches 18; Indels 0
                                                                                                                                                                                                                  0.2-APR-1996 (first entry)
Humanised 5G1.1 VH + IGHRLD DNA.
Complement C5; haemolysis; kidney; glomerulonephritis;
monoclonal antibody; antiinflammatory; antibody engineering;
humanised antibody; complementarity determining region; CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 T;
                                                                                                                                                                                                                                                                                                                                                                                                                     Rollins S;
                                                                                                                                                                                                                                                                                                                                                                                                                                Thomas TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human complement C5a generation and thus to reduce inflammation and kidney dysfunction associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 G;
                                                                                                                                                                                                                                                                                                                                                                                                                      Nye SH,
                                                                                                                                                                                                                                                                                                                                                                                                                  Evans MJ, Matis L, Mueller EE, Nye SH, Rother RP, Springhorn J P, Squinto SP, Walkins JA; WHIKINS JA; P-PSDB; R77615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 C;
                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..750
1..750
1..57
/*tag= a
/*tag= b
/*tag= c
                                                                                                                                   197 CAAGGAACCCTGGTCACTGTCTCGAGC 423
                                                                                                                         CAAGGAACCCTGGTCACTGTCTCGAGC 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 A;
                                                                                                                                                                                                108487 standard; DNA; 750 BP. 108487;
                                                                                                                                                                                                                                                                                                                                                                            09-NOV-1995.
01-MAY-1995; U05688.
02-MAY-1994; US-236208.
(ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 369; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            750 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                mat_peptide
                                                                                                                                                                                                                                                                                 Synthetic.
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538
                   217
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                                                                                 658
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                                        598
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T08487
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358 GGATCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAG 417
                                                                                      597
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A DNA construct (108483) codes for a humanised CDR-grafted and framework sequence-altered Fd 5G1.1 VH + IGHRL (R77610), which includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The DNA can be subcloned together with DNA (708484) coding for a humanised light chain (R77612) into vector APEX-3P (T08476) for expression of humanised antibody in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAD 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with
                                                                                                                                                                                GGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGAC
                                                                                                                                                                                                                                                                         658 IAFTATTGCGCGCGTTATTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR.1996 (first entry)
Humanised 5G1.1 VH + IGHRL DNA.
Complement C5; haemolysis; kidney; glomerulonephritis;
monoclonal antibody; antilnflammatory; antibody engineering;
humanised antibody; complementarity determining region; CDR;
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Thomas TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.9%; Score 350.2; DB 1;
94.1%; Pred. No. 1.6e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Squinto SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 C;
                                                                                                                                                                                                                                                                                                                                                                  744
                                                                                                                                                                                                                                                                                                                                                                                          397 CAAGGAACCCTGGTCACTGTCTCGAGC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1...750
                                                                                                                                                                                                                                                                                                                                                                  718 CAAGGAACCCTGGTCACTGTCTCGAGC
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Rother RP, Springhorn J P,
Wang Y, Wilkins JA;
WWPI; 95-302923/50.
P-PSDB; R77610:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T08483 standard; DNA; 750 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
1. .57
/*tag= b
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/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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01-MAY-1995; U05688.
02-MAY-1994; US-236208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glomerulonephritis.
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Matches 364;
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Query Match
Best Local Similarity 96.0
Matches 336; Conservative
                                                                                                                                                                Treating glomerulonephritis with antibody against complement C5 component - to inhibit complement induced cell lysis Claim 42; Page 129-131; 181pp; English.

A DNA construct (T10706) codes for a humanised CDR-grafted and framework sequence-altered light chain, 5G11 VL + KLV56B (R77613), which includes CDRs derived from mouse anti-C5 monoclonal antibody which includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The DNA can be subcloned together with DNA (T08483) coding for a humanised Fd (R77610) into vector APEX-3P (T08476) for expression of humanised antibody in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-1995.
01-MAY-1995; U05688.
02-MAY-1994; US-236208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanised 5G1.1 VL + KLV56B DNA.

Complement C5; haemolysis; kidney; glomerulonephritis; monoclonal antibody; antiinflammatory; antibody engine humanised antibody; complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang Y, Wilkins J. WPI; 95-392923/50. P-PSDB; R77613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ALEX-) ALEXION PHARM INC.
Evans MJ, Matis L, Mueller
Rother RP, Springhorn J P,
Wang Y, Wilkins JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                           glomerulonephritis.
Sequence 726 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATTATTGCGCGCGTTATTTTTTGGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGT
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1. .75
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76. .723
/*tag= 0
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1. .726
                           44.0%;
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     0
  Score 328.8; DB 1
Pred. No. 1.5e-82;
0; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EE, Nye SH,
Squinto SP,
                                                                                                                             206
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Thomas TC;
                                                                                                                             187
                                                  DB 1;
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region; CDR;
     Indels
                                                  Length
  0
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          597
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P-PSDB; R77614.

P-PSDB; R77614.

Treating glomerulonephritis with antibody against complement C5 recomponent to inhibit complement induced cell lysis component to inhibit complement induced cell lysis?

Claim 35; Page 132-34; 181pp; English.

A DNA construct (T08486) codes for a humanised CDR-grafted light chain, designated 5G1.1 VL + 012 (R77614), which includes colls derived from mouse anti-C5 monoclonal antibody 5G1.1 The DNA can be subcloned together with DNA (T08484) coding for a humanised fd (R77611) into vector APEX-3P (T08476) for expression of humanised antibody in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis.

Sequence 711 BP; 174 A; 206 C; 183 G; 148 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Evans MJ, Matis L,
Rother RP, Springh
Wang Y, Wilkins JA
WPI; 95-392923/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-1995.
01-MAY-1995; U05688.
02-MAY-1994; US-236208.
(ALEX-) ALEXION PHARM IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T08486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-1996 (first entry)
Humanised 5G1.1 VL + 012 DNA.
Complement C5; haemolysis; kidney; glomerulonephritis;
monocional antibody; antiinflammatory; antibody engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCCTGAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGGTTGACTTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody; complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Springhorn
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67. .708
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
1. .66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L, Mueller
nghorn J P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Squinto SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rollins S
Thomas TC;
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Query Match
Best Local Similarity
Matches 331; Conserv

Conservative

43.3%; 96.5%;

Score Pred.

Mismatches 323.8; No. 3.6

.6e-81

몂 ۲,

Length

711; 0;

Gaps

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W09119739-A
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                                                          186
                                                                               186
                                                                                                   246
                                                                                                                                                              306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating glomerulonephritis with antibody against complement C5 component - to inhibit complement induced cell lysis Example 11; Page 126-128; IBIPP; English.

A DNA construct (108485) codes for a humanised CDR-grafted and framework sequence-altered light chain, 561.1 VL + KLV56 (R77612), which includes CDRs derived from mouse anti-C5 monoclonal antibody for a humanised FG (R77610) into vector APEX-3P (T08483) coding for a humanised antibody in human 293 EBNA cells. Such human complement C5a generation and thus to reduce glomerular
           GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT
                                                                                                                                                                     GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT
                                                                                                                               GATATCCAGATGACCCCAGTCCCCGTCCTCCCTGTCCGCCTCTGTGGGCGATAGGGTCACC
                                       ATCACCTGCGCCCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT
                                                                                                                    CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT
                                                                                                                                                             GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 726;
                                                                                                                                                                                                                                                                                         15-MAR.1996 (first entry)
Humanised 5G1.1 VL + KLV56 DNA.
Complement C5; haemolysis; kidney; glomerulonephritis;
monoclonal antibody; antiinflammatory; antibody engineering;
humanised antibody; complementarity determining region; CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ë
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                                                                                                                                                                                                             GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rollins S
Thomas TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human complement C5a generation and thus to reduce inflammation and kidney dysfunction associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 322.4; DB 1;
Pred. No. 8.9e-81;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EE, Nye SH,
Squinto SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 C;
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evans MJ, Matis L, Mueller
Rother RP, Springhorn J P,
Wang Y, Wilkins JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.2%;
95.4%;
                                                                                                                                                                                                                                                                        T08485 standard; DNA; 726 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 A;
                                                                                                                                                                                                                                                                                                                                                                          1. .726
/*tag= a
1. .75
/*tag= b
76 .723
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-1994; US-236208.
(ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 43.2
Best Local Similarity 95.4
Matches 332; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-1995.
01-MAY-1995; U05688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glomerulonephritis.
Sequence 726 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang Y, Wilkins Jr
WPI; 95-392923/50.
P-PSDB; T08485.
                                                                                                                                                                                                                                                                                                                                                                                               signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9529697-A1
                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                  T08485;
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                                                                                                                                                                               307
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                   29
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61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New multivalent antigen-binding proteins - comprise Fv fragment linked to at least 1 other Fv fragment spacer and useful for in-vivo diagnosis or therapy
Example; Fig 5 34pp; English.

Example; Fig 5 34pp; English.

The bivalent antigen-binding protein B72.3 Fv (R20184) is an example of the antigen-binding proteins of the invention. They comprise a first Fv fragment bound to at least one other Fv fragment by a linker which keeps the Fv fragment apart. The connecting structure of R20184 comprises a joining sequence derived from a human IgG1 domain linked to a complete human IgG4 hinge region. R20185 is the sequence of the shortened hinge version of the B72.3 single chain Fv
                                                                                                                                                                                                                                                                                                                                                                                                 AGCCTGAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCG
                                                                                                                             AACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAAACCTGGCAGATGGAGTCC
                                                                                                                                                                                                                                                                                                                            020381;
15-APR-1992 (first entry)
Sequence encoding the shortened hinge version of the B72.3 single
chain Fv hinge.
Fv fragment; in vivo diagnosis; therapy; antibody; ss.
                            4 GCCGATATCCAGATGACCCAGTCCCCGTCTCCCTGTCCGCCTCTGTGGGCGATAGGGTC
                                                                                                 TCACCATCACCTGCGGCGCCAGCGAAACATCTATGGCGCGCTGAACTGGTATCAACGTA
     TGGCCGATATCCAGATGACCCAGTCCCCGTCCTCCTGTCCGCCTCTGTGGGCGATAGGG
                                                                                                                                                                                                                          CITCICGCTICICIGGAICCGGCTCCGGAACGGAITTCACTCTGACCATCAGCAGTCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377 GACAGGGTACCAAGGTGGAAATAAAACGAACTGTGGCTGCCACCATCTG 424
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Pred. No. 7.5e-73;
0; Mismatches 220; Indels
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King DJ, Mountain A, Owens RJ, Yarranton GT;
WPI; 92-024365/03.
P-PSDB; RZ0185.
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Best Local Similarity 66.3%;
Matches 439; Conservative
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11-JUN-1990; GB-012995.
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PN W0930130-A.

PN W0930130-A.

PF 04-NOV-1992; U09487.

PR 04-NOV-1992; US-787567.

PR 19-JUN-1992; US-901707.

PR Analogues of type I ribosome inactivating protein - useful as protein cytotoxic agents, immuno toxins for treating auto immune diseases, pr cytotoxic agents, immuno toxins for treating auto immune diseases, pr cancer, graft versus host disease and selective cell killing in-vivo PS Example 12; Page 123-124; 163pp; English.

CC A single chain antibody form of the has H5 variable domain was casembled from previously constructed genes. This scab segment compared in the entire V and J segment of the other (light or Cheavy) via a 15 amino acid flexible peptide. The scab was assembled con two orientations (see 042284 and 042285). A fusion construct was prepared in which the natural sequence gelonin gene was positioned controlled the N-terminus and the SLT or RMA linker peptide was positioned
                                                                                                                                                                                                                                                                                                                                                        V-J(kappa)/[(Gly)4Ser]37V-J(gamma) single chain antibody.
Type I ribosome-Inactivating protein; ricin; gelonin;
immunoconjugate; autoimmune disease; cell killing; toxin;
overlap extension polymerase chain reaction; H65 variable region;
RMA; rabbit muscle aldolase; cathepsin cleavage;
SLT; E.coli Shiga-like toxin; human engineered antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q42284 standard;
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           Rana pipiens.
Synthetic.
WO9731116-A2.
                                  R. pipiens recompinant name R. ribonuclease; cytotoxic; rNase A; ribonuclease; cytotoxic; tumour cell growth; frog; ss.
                                                                    20-APR-1998
R. pipiens 1
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Sequence
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                                                               P-PSDB; W35125.
Ribonuclease molecules based on native Onconase - used for killing cells, particularly tumour cells
Disclosure; Page 67; 90pp; English.
Sequences 194963 to 194973 encode recombinant fusion proteins (rOnc)
which are modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or too form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also used for cell separation in vitro by selectively killing unwanted types
                                                                                                                                                                                                                                 of cells, e.g. In bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for Killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to none and also
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                                                                                                                                                                                                                                                                                                                                                                                           Length 1065;
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                                                                                                                                                                                                                                                                                                                                                                                         Score 267; DB 1;
Pred. No. 2.7e-65;
                                                                                                                                                                                                                                                                                                                                       252
21-FEB-1996; US-011800.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
BOQUE L. Newton DL, Rybak SM, Wlodawer A;
WPI; 97-435168/40.
                                                                                                                                                                                                                                                                                                                                     240 C;
                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                       lower immunogenicity in humans.
Sequence 1065 BP; 301 A;
                                                                                                                                                                                                                                                                                                                                                                                       35.7%;
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Best Local Similarity
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calls, particularly tumour cells

Disclosure; Page 71; 90pp; English.

Sequences T94963 to T94973 encode recombinant fusion proteins (ronc)

Which are modifications of the RNase Onconase (RTM) (nonc). Such novel

Tibonuclease molecules are highly cytotoxic and can be used alone or

to form chemical conjugates or to target recombinant immunofusions. They

are used particularly for decreasing tumour cell growth. They can also be

used for cell separation in vitro by selectively killing unwanted types

cused for cells, e.g. in bone marrow prior to transplantation into a patient

undergoing marrow ablation by radiation, or for killing leukaemia cells

or T-cells that would cause graft versus host disease. The toxins can

also be used to selectively kill unwanted cells in culture. The new

ribonucleases have increased cytotoxic activity compared to nonc and also

lower Immunogenicity in humans.

Sequence 1065 BP; 301 A; 241 C; 250 G; 273 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribonuclease molecules based on native Onconase - used for killing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCACTTGCAAGGCGAGTCAGGACATTAATAACTATTTATGCTGGTTCCAGCAGAAACCA
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9
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21-FEB-1997; U02588.
21-FEB-1996; US-011800.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
WPI: 97-445168/40.
P-PSDB; W35129.
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Best Local Similarity 63.4%;
Matches 427; Conservative
                                                                                                                                                                                               standard; DNA; 1065
                                                                                                                                                                                                                                                           20-APR-1998 (first entry)
Synthetic.
WO9731116-A2.
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427

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PS Disclosure; Page 69; 90pp; English.

CC Sequences T94963 to T94973 encode recombinant fusion proteins (rOnc)

CC which are modifications of the RNase Onconase (RTM) (nOnc). Such novel

CC ribonuclease molecules are highly cytotoxic and can be used alone or

CC to form chemical conjugates or to target recombinant immunofusions. They

CC are used particularly for decreasing tumour cell growth. They can also be

CC used for cell separation in vitro by selectively killing unwanted types

CC of cells, e.g. in bone marrow prior to transplantation into a patient

CC undergoing marrow ablation by radiation, or for killing leukaemia cells

CC or T-cells that would cause graft versus host disease. The toxins can

CC also be used to selectively kill unwanted cells in culture. The new

CC ribonucleases have increased cytotoxic activity compared to nonc and also

CC lower immunogenicity in humans.

SO Sequence 1074 BP; 304 A; 246 C; 250 G; 274 T;
                                                                                                                                                                                                                      Query Match
Best Local S
Matches 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribonuclease molecules based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boque L, Newton DL, WPI; 97-435168/40. P-PSDB; W35127.
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21-FEB-1996; US-011800.

(USSH) US DEPT HEALTH &
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W09731116-A2.
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                                                                                                                            67
                                                                                                                                                                                           7
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ase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
nour cell growth; frog; ss.
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                              GGGAAATCTCCTAAGACCCTGATCTATCGTGCAAACAGACTGGTAGATGGGGTCCCATCA
                                                                                                                                                      TCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTTTCCAGCTACTGGATGCACTGG
 CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT
                                                                                           TTCACTTGCAAGGCGAGTCAGGACATTAATAACTATTTATGCTGGTTCCAGCAGAAACCA 474
                                                                                                               ATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCGCTGAACTGGTATCAACGTAAACGT 126
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                                                            GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT 186
                                                                                                                                                                                                                       427;
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k SM, w
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                                                                                                                                                                                                                                   DB 1;
.7e-65;
                                                                                                                                                                                                                      240;
                                                                                                                                                                                                                                                   Length 1074;
                                                                                                                                                                                                                      Indels
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Solutions particularly tumour cells

Solutions particularly tumour cells

Sequences 794963 to 794973 encode recombinant fusion proteins (rOnc)

Complete the protein particularly control proteins (rOnc)

Complete the protein particularly control protein pro
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19-FEB-1997; U02588
21-FEB-1996; US-011
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R. pipiens r
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W09731116-A2.
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                                                                      187 CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT 246
                                                                                                                                         GAAGACTICGCIACGIATIACIGICAGAACGITITIAAAIACICCGIIGACITICGGACAG 306
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                                                                                              127 GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT 186
         Gaps
                         GATATCCAGATGACCCAGTCCCCGTCCTCCTGTCGCCCTCTGTGGGCGATAGGGTCACC 66
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Pred. No. 2.7e-65;
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Best Local Similarity 63.4 Matches 427; Conservative
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Search completed: September 12, 2000, 21:01:09 Job time: 3578 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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747
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/cgnl_7/ptodata/1/ina/5B_COMB.seq:*
/cgnl_7/ptodata/1/ina/5C_COMB.seq:*
/cgnl_7/ptodata/1/ina/5C_COMB.seq:*
/cgnl_7/ptodata/1/ina/5C_COMB.seq:*
/cgnl_7/ptodata/1/ina/PCTUS_COMB.seq:*
/cgnl_7/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                          Length
   US-08-488-113B-89
US-08-464-360-89
US-08-646-360-89
US-08-68-65-811-40
US-08-875-811-40
US-08-875-811-46
US-08-875-811-46
US-08-875-811-46
US-08-875-811-42
US-08-875-811-42
US-08-230-843-3
US-08-230-843-3
US-08-224-591-17
US-08-224-591-17
US-08-226-789-17
US-08-26-789-17
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US-08-400-115-3
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215.8	215.8	215.8	216.2	216.2	216.2	218	220.6	220.6	221.8	223.2	224.4	224.4	230.6	230.6	230.6	230.6	230.6	230.6
28.9	28.9	28.9	28.9	28.9	28.9	29.2	29.5	29.5	29.7	29.9	30.0	30.0	30.9	30.9	30.9	30.9	30.9	30.9
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Sequence 3, Appli	ω	Sequence 3, Appli	Sequence 18, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 1, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 1, Appli	Ļ	۳	Sequence 5, Appli	Sequence 5, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 6, Appli	Sequence 6, Appli

## ALIGNMENTS

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TELEX: 904136
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 819 base pairs
TYPE: nucleic acid
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Patent No. 5864019
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/842,193 FILING DATE: 17-MAR-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/400,115
FILING DATE: 06-MAR-1995
PRIOR APPLICATION UNMBER: US 08/127,136
FILING DATE: 27-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9012995.8
FILING DATE: 11-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OWENS, Raymond John
APPLICANT: YARRANTON, Geoffrey Thomas
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MOUNTAIN, Andrew APPLICANT: OWENS, Raymond JAPPLICANT: YARRANTON, Geoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                               NAME: ISACSON, John P. REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/
FILING DATE: 11-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: Foley & Lardner I: 3000 K Street, N.W Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Release #1.0, Version #1.25
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NUMBER OF SEQUENCES:
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US-07-988-430-92
Sequence 92. Application US/07988430
Sequence 92. Application US/07988430
GENERAL INFORMATION:
APPLICANT: Bether, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Let, Shau-Ping
APPLICANT: Let, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
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                                                                                                                                                                        64 GCTGATATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGTATCTGTGGGAGAAACTGTC 123
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                                                                                                                                                                                                                                    124 ACCATCACATGTCGAGCAAGTGAGAATATTTACAGTAATTTAGCATGGTATCAACAGAAA 183
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                                                                                                       Length 819;
                                                                                                    Score 294; DB 3;
Pred. No. 2.6e-84;
0; Mismatches 220
                                                                                                       39.48;
66.38;
                                                                                                                   Best_Local Similarity 66.3
Matches 439; Conservative
  double
                                       CDS
1..816
                linear
STRANDEDNESS:
TOPOLOGY: lin
FEATURE:
                                     ; NAME/KEY:
; LOCATION:
US-08-400-115-3
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TG 722
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                                                                                                       Query Match
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                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FLIANG DATE: 19921209
CLASSIFICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION NUMBER: US 07/91,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-UN-1991
ATTORNEY/AGENT INFORMATION:
NAMME: NO. 5416202and, Greta E.
REGISTRATION NUMBER: 31333
TELECOMMUNICATION NUMBER: 31333
TELECOMMUNICATION NUMBER: 3133
TELECOMMUNICATION NUMBER: 3120
TELER: 25-3856
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHRRACTERISTICS:
TENGTH: 723 base pairs
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 283.4; DB 1;
Pred. No. 5.8e-81;
0; Mismatches 251;
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Best Local Similarity 63.7%;
Matches 472; Conservative (
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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US-07-988-430-92
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                                                                                                                                                CITY: Chicago
STATE: Illinois
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US-08-425-336-89
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GENERAL INFORMATION:
                                                                                                                                                                                       FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION UNMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NUMBER: MEYETS: THOMAS C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Inmunotoxins
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                              INFORMATION FOR SEQ ID NO:
                           SEQUENCE CHARACTERISTICS
                                                                                                                     NAME: Meyers, Thomas C.
REGISTATION NUMBER: P-36,9
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                  TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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     base pairs
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Tower, 233
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                                                                            US-08-488-113B-89; Sequence 89, Application; Patent No. 5744580; GENERAL INFORMATION:
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; STRANDEDNESS: sing:
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-425-336-89
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   APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxi
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Immunotoxins Comprising Ribosome-Inactivating
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Pred. No. 5.8e-81;
0; Mismatches 251
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Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Betrer, Marc D.
APPLICANT: Studiks, Gary M.
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                         GGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCCGAGGTCAAGAAGCCAGGGGCC
                                                                                                                                                                       355 GGTGGAGGATCTGAGATCCAGTTGGTGCAGTCTGGAGGAGGCCTGGTGAAGCCTGGAGGG
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                                                                                                                                                                                                                                                          415 TCCGTCAGAATCTCCTGCGCAGCTTCTGGGTATACCTTCACAAACTATGGAATGAACTGG
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                                                                                   GGCACCAAGCTTGAGATGAAA-----GGTGGCGGTGGATCTGGTGGAGGTGGGTCCGGA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIALE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREWY APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
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500 West Madison Street, 34th floor
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APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
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STATE: Illinois
COUNTRY: USA
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US-08-477-484B-89
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Pred. No. 5.8e-81;
0; Mismatches 251; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MCNICALIAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEFORM: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                           ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                           CURENT APPLICATION DATA:
CURENT APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
RICH APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY-AGENT INFORMATION:
NAME: MACHICALIOR
                                                                                                                                                                ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
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63.78;
TITLE OF INVENTION: Proteins
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                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: sing
                                                                               STREET: 500 West
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Best Local Similarity
Matches 472; Conserv
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Best Local Similarity
Matches 472; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
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FILING DATE: 04 NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEPHAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-JUN-1992 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
                  GCGCGTTATTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTTGGGGTCAAGGAACC 726
                                                                                                                                                                                                                                                                                                                                                                                         GGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCGCGAGGTCAAGAAGCCAGGGGCC 426
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ACAAGACGGGGTTACG-----
                                                                      AACACTGCCTATTTACAGATCAACAGCCTCAGAGCCGAGGACACGGCTGTGTATTTCTGT 654
                                                                                         AGTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGC 666
                                                                                                                                            GAGCCAACATATGCTGATTCTTTCAAGGGACGGTTTACCTTCTCTTTGGACGATTCTAAG
                                                                                                                                                                    AGCACCGAATATACCGAAAATTITAAAGACCGTGTTACTATGACGCGTGACACTTCGACT 606
                                                                                                                                                                                                                                                      GTGCGTCAGGCCCCGGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGT 546
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                                                                                                                                                                                                                      GTGCGCCAGGCTCCAGGAAAGGGTTTAGAGTGGATGGGCTGGATAAACACCCCACACTGGA 534
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Pred. No. 5.8e-81;
0; Mismatches 251;
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                                                                   Matches 472;
                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 0///-
APPLICATION NUMBER: US 0///-
PILING DATE: 04-NOV-1991
ATTORNEY/ACENT INFORMATION:
NAME: MCNIcholas, Janet M.
NAME: MCNIcholas, Janet M.
200-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
                                                                                                                                                                                                                                                                         TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELES: 650 388-1248
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PCT/
FILING DATE: 12-MAY-1994
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Better, Marc D. APPLICANT: Carroll, Stephen APPLICANT: Studnika, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 500 W
                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 32,
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               GATATCCAGATGACCCAGTCCCCGTCCCTGTCCGCCTCTGTGGGGGGATAGGGTCACC 66
GACATCCAGATGACTCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGAGACAGAGTCACT
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5. 5837491
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500 West Madison Street, 34th floor
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                                                                 Score 283.4; DB 3;
Pred. No. 5.8e-81;
0; Mismatches 251;
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GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Betrer, Marc D.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bickell
                                                            366
                                                                                                                                                                                                                                                                                           486
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ATCACCTGCGGCGCCAGCGAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
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STREET: Street
CITY: Chicago
STATE: Illinois
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MEDIUM TYPE: Floppy disk
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COUNTRY: USA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.9%; Score 283.4; DB 6; Best Local Similarity 63.7%; Pred. No. 5.8e-81; Matches 472; Conservative 0; Mismatches 251;
                                                                                                                              FILING DATE: 19921104
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      NAME: Noland, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 3112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 723 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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RESULT 8
US-08-875-811-40
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                                                                  US-08-875-811-40
Query Match
Best Local Similarity
Matches 427; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40,
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Rybak, Susanna
APPLICANT: Newton, Dianne
APPLICANT: Boque, Lluis
                                                                                                                                                                                                               TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: WO PO FILING DATE: 19-FEB-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60 FILING DATE: 21-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wlodawer, Alexander TITLE OF INVENTION: Recombinant Ribonuclease Proteins NUMBER OF SEQUENCES: 64
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Sa
STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      607
                                                                               NAME/KEY: CDS
LOCATION: 1..1065
OTHER INFORMATION:
                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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6045793
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Two Embarcadero
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 Conservative
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                                                                                                                                                            single
             35.7%;
63.4%;
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                                                                               /note= "sfvfBMetGluOnc"
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            Score 267; DB 5; Pred. No. 1.2e-75;
 Mismatches
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 240;
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                        Length 1065;
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Gaps
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US-08-875-811-48
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                                                                                                                                                                                                                                                  Sequence 48, Patent No. 6
                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                         APPLICANT: Rybak, Susani
APPLICANT: Newton, Diani
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Ali
TITLE OF INVENTION: Reconumber OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
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                                                              COUNTRY:
ZIP: 941
                                                                                       STREET: Two Embarcac
CITY: San Francisco
STATE: California
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                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                 ACCCCTCTTATT
                                                                94111-3834
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6045793
                                                                                                                  Two Embarcadero
                                                                               USA
                                                                                                                                                                                                Newton, Diani
Boque, Lluis
                                                                                                                              Townsend and
                                                                                                                                                                                                                           Susanna
                                                                                                                                                                                                           Susanna M.
Dianne L.
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                                                                                                                  Center, E
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COMPUTER READABLE FORM:
MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCC
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                                                                                                                                                                                                                                                                                                                                Wlodawer, Alexander
WENTION: Recombinant Ribonuclease Proteins
                                                                                                                                                                                                                                        d and Crew LL
Eighth Floor
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67 ATCACCTGCGCCCCAGCGAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
                                        7 GATATCCAGATGACCCAGTCCCCGTCCTCCTGTCGCCCTCTGTGGGCGCATAGGGTCACC 66
                     AGTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGC
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                                                                                                                                                                                                                                           Sequence 44, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Modawer, Lluis
APPLICANT: Widdawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEADELIN PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAM:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
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Two Embarcadero Center, Eighth Floor
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APPLICATION NUMBER: W0 PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                       667 GCGCGTTATTTT 679
                                                                                                                                            655 ACCCCTCTTATT 667
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; OTHER INFORMATION:
US-08-875-811-44
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US-08-875-811-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCC 426
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                                                 PRIOR APPLICATION: 453

RIOR APPLICATION ADARS:
APPLICATION NUMBER: W0 PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
TYPE: nucleic acid
STRANBONESS: single
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ilarity 63.4%;
Conservative (
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Best Local Similarity
Matches 427; Conserv
                       FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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Sequence 50, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ri
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
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                                                                     COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                 STREET: Two Embarca
CITY: San Francisco
STATE: California
                            CLASSIFICATION:
                                             APPLICATION NUMBER: US/08/875,811 FILING DATE: 19-FEB-1998
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INFORMATION FOR SEQ ID NO: 50
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 427; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY_AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REGISTRATION NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA
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LOCATION: 1..1074
OTHER INFORMATION:
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                            AGTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGC
                                                           AGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACT
                                                                                                                        ATAAAACAGAGCCTGGACAGGGTCTGGACTGGATTGTCGCTATTGATCCTCGAAATAGT
                                                                                                                                                       GTGCGTCAGGCCCCGGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGT
                                                                                                                                                                                    GCGGCGGCTCTGAGGTTCAGCTCCAGCAGTCTGGGACTGTACTGGCAAGGCCTGGGGCT
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63.4%;
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955 AGCACTGCCTACATGGAACTCAACAGCCTGACAATGAGGACTCTGCGGTCTATTACTGT 1014
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481 GGGAAATCTCCTAAGACCCTGATCTATCGTGCAAACAGACTGGTAGATGGGGTCCCATCA 540
                                                                                                                                                                                                                                                                                                                                                       661 GGGACCAAGCTGGAAATAAAA----GGAGGCGGTGGCTCGGGCGGTGGCGGATCGGGT 714
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                                                             187 CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT
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APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wiodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
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PAPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
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APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Pred. No. 1.2e-75;
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                                                                                                                                                                                                 Sequence 46, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Modawer, Lluis
APPLICANT: Modawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 21-FEB-1996
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATORNEY/AGENT INFORMATION:
NAME: FALIS, SUSAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELEPHONE: (415) 576-0200
TELEPRAX: (416) 57
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STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
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MEDIUM TYPE: Floppy
                                                          1009 ACCCCTCTTTATT 1021
   667 GCGCGTTATTTT 679
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US-08-875-811-46
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-08-875-811-46
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TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPB: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local :
1081 ACCCCTCTTTATT 1093
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                                                                                                                   GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG
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                                                       AGCACCGAATATACCGAAAATTTTAAAAGACCGTGTTACTATGACGCGTGACACTTCGACT 606
                                                                                                                                                                             ATAAAACAGAGGCCTGGACAGGGTCTGGACTGGATTGTCGCTATTGATCCTCGAAATAGT
                                                                                                                                                                                             GTGCGTCAGGCCCCGGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGT 546
                                                                                                                                                                                                                                      GGCGGCGCTCTGAGGTTCAGCTCCAGCAGTCTGGGAACTGTACTGGCAAGGCCTGGGGCT
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63.4%;
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Pred. No. 1.2e-75;
D; Mismatches 240;
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US-08-230-843-3
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US-08-230-843-3
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TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 base pairs
                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 447; Conserv
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Patent No. 5582826
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FILING DATE: 21-APR-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 094491/1993
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 036065/1994
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: ODION, NO. 5582826man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: IMMUNOSUPPRESSANT NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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NAME/KEY:
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ADDRESSEE: P.C.
ADDRESSE: 1755 S. J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1755 S. CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
124
                                  127
                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: PatentIn Release
                                                                    54
                                                                                                    67
                                                                                                                                    4
                                                                                                                                                        7 GATATCCAGATGACCCAGTCCCCGCCTCTCTCCGCCTCTGTGGGCGATAGGGTCACC
                                                                                                                                      GATATTCTGCTGACACAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTCACC 63
GGAAAATCTCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGGTGTGCCATCA 183
                              GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT 186
                                                                                           ATCACCTGCGGCGCCAGAAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
                                                                    ATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTATCAGCAGAAACAG
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KANAYAMA, YUKA
SUGAMURA, KAZUO
TAKESHITA, TOSHIKAZU
                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                        Score 250; DB 1;
Pred. No. 2.5e-70;
                                                                                                                                                                                                                                                                                                                                                                 acid
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                                                            GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT 246
                                                                            415 TCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCACAGCCTACATGGAGCTCCACAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGT 654
                                                                                                                                         547 AGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACT
                              184 AGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAGCCT
                                                                                                                         GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTGGTGGCGGTGGATCTGGT
                                                                                                                                                                                   367 GGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTKI.

Z1P: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COUNTRY PATEME PATEME RELEASE #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SHIMMURA, TOSHIRO
APPLICANT: HAMDRO, JUNJI
APPLICANT: NAKAZAWA, HARUMI
APPLICANT: SUGAMURA, YUKA
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/636,936
FILING DATE: 24-APR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/230,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08636936 Patent No. 5856140 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 GGGACCAAGCTGGAGCTCAAA-----GTCGAGAAATCCTCAGGATCTGGCTCCGAA 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 GATATITCIGCIGACACAGICICCAGCCICCCTAICTGCATCTGTGGGGAGAAACTGICACC 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       547 AGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT
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                APPLICATION NUMBER: JP 094491/1993
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 036065/1994
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, NO. 58561440man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0674-0X
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
21-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 33.5
Best Local Similarity 60.9
Matches 447; Conservative
  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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US-08-636-936-3
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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1: gb_ba1:
2: gb_ba2:
  972840 seqs, 892348106 residues
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Gapop 10.0 , Gapext 1.0
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750
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9b_pat:*
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o number of sec	_vi	b_v11	b htg3	b_htq3	b_htq	p_ht	b_htg2	b_htg	b_htg	b_htg	b_htg	ţ	p_ht	p_ht	_htg	ե_հէ	'n	g	, L	ğ	m_htg	b_htg	gb_htg16:*	_h_հէ	ni_d	디	שלי	שלי	ļ	ļ	片	յ <mark>ել հ</mark> ե	pr5	$\vdash$		_htg	ř		gb_htg7:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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24	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	σ	v	4	ω	N	_	. o	It.
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756	6557	687	671	2178	2178	762	762	762	762	13254	13254	13254	13254	3282	3282	3282	3282	18986	9209	9209	9209	1599	Match Length	
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AB022655 Homo sapi I69461 Sequence 29	I26929 Sequence 3	I65402 Sequence 1	AF051100 Homo sapi	AR054190 Sequence	AR048108 Sequence	I87063 Sequence 57	179289 Sequence 57	I73104 Sequence 57	I69485 Sequence 57	I58610 Sequence 17	I58596 Sequence 15	AR038321 Sequence	AR038307 Sequence	I58609 Sequence 16	I58595 Sequence 15	AR038320 Sequence	AR038306 Sequence	AR051652 Sequence	AR060920 Sequence	AR015961 Sequence	AR000007 Sequence	м87789 Human (hybr	Description	

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182. .196
//gene="CDR1"
./note="complementarity-determining region 1; putative"
239. .289
//gene="CDR2"
239. .289
                                                                                                                                                                                                note="complementarity-determining region 3; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TGTAAAGCTAGCGGCTATATTTTTCTAATTATTGGATTCAATGGGTGCGTCAGGCCCCC 180
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                                                                                                                                      /note="complementarity-determining region 2; 386. .439
                                                                                                                                                                                                              386. 439
479.me="CoDR3"
7.note="constant region; putative"
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Pred. No. 7.6e-103;
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/note="putative"
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KDTLMISRPEVTCVVVDVSHEDPEYKFNWYVDGVEVHNAKTKPREEGYNSTYRVVSY
LTTLHQDWLNGKEYKCKVSVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQY
SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSFWQOGN
VFSCSVMHEALHNHYTQKSLSLSPGK"
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ISLASEDTAVYYCARDYRCANFRARVGWFDPWGGGTLVTVSSASTRGPSVPPLAPS
SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
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Human (hybridoma H210) anti-hepatitis A IgG variable region,
constant region, complementarity-determining regions mRNA, complete
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Lewis, A.P., Lemon, S.M., Barber, K.A., Murphy, P., Parry, N.R., Peakman, T.C., Sims, M.J., Worden, J. and Crowe, J.S.
Rescue, expression, and analysis of a neutralizing human anti-hepatitis A virus monoclonal antibody
J. Immunol. 151 (5), 2829-2838 (1993)
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/note="Anti-hepatitis A; putative"
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/product="IgG"
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REFERENCE AUTHORS

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           GGGGGCACAGCGGCCTGGGCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTG
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GGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTG
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1 (bases 1 to 9209)
Anderson, D.R., Hanna, N.,
Rastetter, W.H.
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Therapeutic application
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Pred. No. 2.5e-102;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown.
Unclassified.
1 (bases 1 to 9209)
Anderson.D.R., Hanna,N., Leonard,J.E., Newman,R.A., Reff,M.E. and
Rastetter,W.H.
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              1938 TCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACCTCCCGGCTGTCCTACAGTCC 2997
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421 AGCGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAAGAGCACCTCT
                                                 GGGGGCACAGCGGCCCTGGGCTGCTCAAGGACTACTTCCCCGAACCGGTGACGGTG
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Sequence 3 from patent US 5843439.
AR060920 GI:5988611
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2397 c 2390 g
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Unclassified.

[ (bases 1 to 18986)

Reff.M.E., Barnett,R.Spence and McLachlan,K.Retta.

Method for integrating genes at specific sites in mammalian cells
via homologous recombination and vectors for accomplishing the same
Patent: US 5830698-A 2 03-NOV-1998;
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AR051652.1 GI:5975016
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Sequence
AR038306
AR038306.
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1 (bases 1 to 3282)

Burton,D.R., Barbas,C.F. and Lerner,R.A.
Human neutralizing monoclonal antibodies
                                                                                  h 62.3%;
Similarity 78.7%;
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Db 3208 GITCAGCIGGITCAGICGGGGCIGAGGIGAAGAAGCCIGGGGCCICAGIGAAGGITICI 3149	Qy 1 ATGAAGTGGAGC
121 IGTAAAGCTAGCGGCTATATTTTTTTATATGGATTCAATGGGTGCGTCAGCCCCC	15
DD 3148 TGTCAGGCTTCTGGATACAGATTCAGTAACTTTGTTATTCATTGGGTGCGCCAGGCCCCC 3089	Qy 61 GTCCAACTGGTG
GGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGGCTCTGGTAGCACCGAATATACC	75
3008 GGACAGAGGIITGAGIGGAIGGGAIGGAICCAACCITACAACGGAAACAAGGAITITCA	121
241 GAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACTAGTACAGTG	135
3028	Qy 181 GGGCAGGGCCTG
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2548 GACAAGAAGTIG	646
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REFERENCE 1 (bases 1 to 3282) AUTHORS Burton, D. R., Barbas, C.F. and Lerner, R.A. TITLE Human neutralizing monoclonal antibodies to human immunodeficiency virus	158609 158609.1
Patent: US 5652138-A 154 29-JUL-199 Location/Qualifiers e 13282 /organism="unknown"	Σ
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Burton,D.R., Barbas,C.F. and Lerner,R.A.
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Location/Qualifiers
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Pred. No. 2.7e-100;
0; Mismatches 141;
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1 (bases 1 to 13254)
Burton,D.R., Barbas,C.F. and Lerner,R.A.
Human neutralizing monoclonal antibodies
                                                                                                 Patent: US 5804440-A 170 08-SEP-1998
                                                                                                            Location/Qualifiers
1. .13254
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Burton,D.R., Barbas,C.F. and Lerner,R.A.
Human neutralizing monoclonal antibodies
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Location/Qualifiers
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Burton,D.R., Barbas,C.F. and Lerner,R.A.
Human neutralizing monoclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus
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Similarity 78.7%;
77; Conservative
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Pred. No. 2.7e-100;
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169485
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Frong, S., Hebert, C.Alice, Kim, K.Jin a
Anti-IL-8 antibody fragments
Patent: US 5677426-A 57 14-CCT-1997;
Location/Qualifiers
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Doerschuk, C.M., Fong, S., Hebert, C.Alice, Kim, K.Jin and Leong, S.R. Methods for treating bacterial pneumonia
Patent: US 5686070-A 57 11-NOV-1997;

Location/Qualifiers
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Pred. No. 1.9e-98;
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76.8%;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	103676 UI-HE	04759 UVU-HT	104/30 UI-RE	381291 RCO-HT	03588 UI-HF-	506291 QVO-HT	02051 UI-HF-	77689 RC1-CT	06367 QVO-HT	325 QVO-HT	03670 UI-HF-	75944 RCO-CT	03803 UI-HF-	08074 UI-HF-	)2666 UI-HF-BK	30979 CM2-HT	74672 MR1-CT00	70 RC-BT105	33595 PMO-HT	04044 UI-HF-BL	78814 PMO-HT02	7695 RC1	36364 QVO-HT03	76081 RC2-CT02	111 UI-HF-	952 UI-HE-	40 UI-HF	734 UI-HE-	06702 UI-HF-BL	51514 1LZ-CT	205 CM-BIL	000 TOO	999/ RCO-BI	TO CT+00	TH-SAD SCOOL	0543 QVU-HT	2081 UI-HF-	80270 IL2-HT	09631 QVO-ST	093 UI-HF-	0512	04187 UI-HF-BL	7483 wel4a04	360124 EST694
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## ALIGNMENTS

16-FEB-2000 CDNA CLONE	
EST 16- Homo sapiens CD	
AW403676 489 bp mRNA EST 16-FEB-2000 UI-HF-BKO-abh-c-03-0-UI.rl NIH_MGC_36 Homo sapiens cDNA clone	
489 bp -abh-c-03-0-UI 6237 5', mRNA	
AW403676 UI-HF-BKO TMAGE:3056	
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOHNAL	FEATURES	BASE COUNT ORIGIN Query Match Best Local Matches 42	Qy 252 Db 5	Oy 312 Db 65	Oy 372 Db 125	Qy 432 Db 176	Qy 492 Db 236	Qy 552 Db 296	Qy 612
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TCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACT
                                       CAACGTGAATCACAAGCCCAGCAACACCCAAGGTGGACAAGAAGTTGAGCCCCAAATCTTG
                                                                  CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-HT0366-
280100-088-b12&t3=2000-01-28&t4-1)
Seq primer: puc 18 forward
High quality sequence stop: 661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
On May 7, 1998 this sequence version replaced gi:3118821.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao F
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QV0-HT0366-280100-088-b12 HT0366
AW606355
AW606355.1 GI:7311096
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Fax: +55-11-2707001
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The FAPESP/LICR Human Cancer Genome Pr
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1 (bases 1 to 669)
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                                                                                                                                                                                                                       /note="Organ: head_neck; vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/clone_lib="HT0366"
/dev_stage="Adult"
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Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov_bbrp/image/image.html
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UI-HF-BLO-acd-h-05-0-UI.rl NIH_MGC_37
IMAGE:3058808 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Stra
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
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                                                                                                                          -bio.llnl.gov/bbrp/image/image.html
primer: Ml3 Forward
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3058808"
                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg, Ph.D.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0225"
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80.3%;
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                            Tel: +55-11-2704922
Fax: +55-11-2707001
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                                                       /note="Vector: pr773-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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PM2-HT0225-031299-003-b01 HT0225 Homo sapiens CDNA, mRNA sequence.
AW378707
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 581)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
On Feb 10, 1999 this sequence version replaced gi:4061421.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.
                                                                                                                                                                                                  Length 564;
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              /cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LT1)"
                                                                                                                                                                                                                                65;
                                                                                                                                                                                               Score 355; DB 72;
Pred. No. 3.3e-90;
0; Mismatches 65;
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Best Local Similarity 84.8%;
Matches 413; Conservative
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/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMZ&t2=PMZ-HT0225-031299-003-b01&t3=1999-12-03&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 575.
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                                                                         GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG
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On May 18, 1998 this sequence version replaced Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.bb/scripts/gethtml2.pl?t1=RCO&t2=RCO-HTO298-
20119-011-f08&t3=1999-11-20&t4=1)
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Fax: +55-11-2707001
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HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICE Human Cancer Genome Project
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
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AW403588
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Tel: (301) 496-1550
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/cell_line="MGC85"
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/lab_host="DH10B (LTI)"
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/note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;
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Pred. No. 8.7e-88;
0; Mismatches 21;
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Eukaryota: Metazoa: Primates: Catarrhini; Hominidae: Homo.
Manmaliai: Eutheria: Primates: Catarrhini; Hominidae: Homo.

1 (bases 1 to 566)

2 HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
On Jun 15, 1998 this sequence version replaced gi:3224227.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-HT0366-
270100-087-a02&t3=2000-01-27&t4=1)
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QVO-HT0366-270100-087-a02 HT0366 Homo sapiens cDNA, mRNA sequence.
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High quality sequence start: 21
High quality sequence stop: 566
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (base) 1 to 527)

S NIH-MCC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
On Feb 24, 1999 this sequence version replaced gi:4058273.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
DNA Sequencing by: M. B. Soares Lab
Clone distribution: MGC. Conce distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
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/db_xref="taxon:9606"
/clone="IMAGE:3054345"
/clone_lib="NIH_MGC_36"
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/cell_type="germinal center B
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Seq primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352;
         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-CT0199-
100999-021-A07&t3=1999-09-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 32
High quality sequence stop: 442.
                                                                                                                                                                                                                  The FAPESP/LICR Human Cancer Unpublished (1999)
On Apr 3, 1998 this sequence Contact: Simpson A.J.G.
                                                                                                                                                                        Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 442)

HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LICR Human Cancer Genome Project
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AW177689.1 GI:6443726
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Location/Qualifiers
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                                                                                                                                              HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
On May 7, 1998 this sequence version replaced
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01505
                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                 AW606367 634 bp mrNA EST 23-WAR-2000 QV0-HT0366-280100-088-h06 HT0366 Homo sapiens CDNA, mrNA sequence. AW606367 GI:7311108
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QVO&t2=QVO-HT0366-280100-088-h06&t3=2000-01-28&t4-1)
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1 (bases 1 to 634)
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a 123 c 152 g 89 t
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/dev_stage="Adult"
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/db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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primer: puc 18 forward

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94
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AUTHORS
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                                1. .634
/organism="Homo sapiens"
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/dlone_lib="HT0366"
/dlov_stage="Adult"
/dev_stage="Adult"
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Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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QVO-HT0366-280100-088-b09_1 HT0366 Homo sapiens cDNA, mRNA
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8
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                                                                                                                                                                                                                               Score 333.6; DB 74;
Pred. No. 4e-84;
0; Mismatches 149;
           sequence stop: 633
sequence start: 7
                      Location/Qualifiers
                                                                                                                                                                                                                                44.58;
74.28;
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quality
            quality
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Matches 451;
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/dev_stage="Addult"
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Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.
14 a 155 c 116 g 90 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-HT0366-280100-088-b09_lat3=2000-01-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 455.
                                                                                                                                         Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homc 1 (bases 1 to 455)
HGGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project Onpublished (1999)
On May 7, 1998 this sequence version replaced gi:3118791.
Contact: Simpson A.J.G.
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Pred. No. 5.7e-
0; Mismatches
AW606325
AW606325.1 GI:7311066
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Best Local Similarity 90.7%;
Matches 362; Conservative
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AGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACAT 409

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REFERENCE
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Best Local Similarity
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250
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                                                                                                                                                                                                                                                                                                                    10 GACAAGTCCATCAACACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCC 69
                                                                                                                                                        GGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
                                                                                                CCATCGGTCTTCCCCCTGGCGCCCTCCTCCAAGAGCACCTCTGGGGGGCACAGCGGCCCTG 498
                                                                                                                                                                              TATTITGATGTITGGGGTCAAGGAACCCTGGTCACTGTCTCGAGCGCCTCCACCAAGGGC 438
                                                                                                                                                                                                                                        ATGTATTACTGTGCGAGACATGGGTTCCCAGATTGTAGTACCAGCTGCTATGGGTGG 129
                                                                                                                                                                                                                                                                               GTCTATTATTGCGCGCGTTATTTTTTTGGTTCTAGCCCGAAT------TGG 378
                                     GGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCC 558
                                                                            CCATCGGTCTTCCCCCTGGCGCCCCTGCTCCAGGAGCACCTCTGGGGGGCACAGCGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECO RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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1. (bases 1 to 579)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B (LTI)"
/lab_host="DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

a 207 c 150 g 101 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:3056189"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_tine="MGC85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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81.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                Score 322; DB 72;
Pred. No. 7.5e-81;
0; Mismatches 70;
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1 (bases 1 to 442)
1 (bases 1 to 442)
1 HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
On Jul 8, 1999 this sequence version replaced gi
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC2st2=RC0-CT0201-
270999-011-e04&t3=1999-09-27&t4=1)
Seq.primer: puc 18 forward
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RCO-CT0201-270999-011-e04
AW375944
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High quality sequence stop: 442.
Location/Qualifiers
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Fax: +55-11-2707001
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                                                                            Conservative
                                                                                                                                                                                              78
                                                                                                                                                                                          /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

a 106 c 166 g 92 t
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                    /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="CT0201"
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                                                                                              42.8%;
99.4%;
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                                                                                            Score 320.8; DB 71; Pred. No. 1.5e-80;
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04 CT0201 Homo sapiens
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379 TATTTTGATGTTTGGGGGTCAAGGAACCCTGGTCACTGTCTCGAGCGCCTCCACCAAGGGC
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/organism="Homo sapiens"
/db_aref="taxon:9606"
/clone="lymb"
/clone="lymb"
/cell_type="germinal center B cells"
/
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
UNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.blo.llnl.gov/bbrp/image/image/image.html
Seq primer: M13 Forward
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 504)
MIH-MCG http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AW403803 GI:6922847
                                                                                                                                                                                                                                                                       GACTCTACTCCCTCAGCAGCGTGGTCACCGTGCCCTCCAGCATGGGCACCCAGACCT
                                                                                                                                                   GGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG
                                                                                                                                                                                                                                                                                                                                   262 GACTCTACTCCCTCAGCAGCCTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCT
                            GCACAGCGGCCCTGGGCTGGTCAAGGACTACTTCCCCGGAACCGGTGACGGTGTCGT
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Pred. No. 5.9e-80;
0; Mismatches 22; I
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92.6%;
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AUTHORS
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases to 446)

National Institutes of Health, Mammalian Gene Collection (MGC)

In Inpublished (1999)

On Jan 6, 2000 this sequence version replaced gi:6677128.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenin.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CLONA Library Preparation: M.B. Soares Lab

Clone distribution: M.C. Clone distribution information can be found through the I.M.A.G. E. Conscrtium/LINL at:

www-bio.llnl.gov/bbry/image/image/image.html

Seq primer: M.B. Soares.html
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AW408074 GI:6927131
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/tissue_type='lymph"
/cell_type='germinal center B cells"
/cell_line="MGG85"
/lab_host="DH10B_(III)"
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/db_xref="taxon:9606"
/clone="IMAGE:3062802"
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                                                 Query Match
42.5%; Score 318.6; DB 72; Length 446;
Best Local Similarity 88.3%; Pred. No. 6.5e-80;
Matches 361; Conservative 0; Mismatches 39; Indels 9;
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Search completed: September 12, 2000, 20:04:56 Job time: 3493 sec

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OM nucleic - nucleic search, using sw model
Total number of hits satisfying chosen parameters:
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Perfect score:
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                                            311585 seqs, 125096042 residues
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Gapop 10.0 , Gapext 1.0
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750
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                                                                                                                                                                                                                                                                                                                                                                             GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
        623170
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Database : N_Geneseq_36:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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V06414 V10293	T93546 V03207	T03364	T15932 Q43844	092547	T62938 T15202
Chimeric monoclona Mab 5.12.14 and hu	Chimeric monoclona Murine variable an	Anti-IL-8 MAb 5.12 Chimeric monoclone	Anti-IgE VH expres Plasmid pAH4602. <i>P</i>	Expression vector,	3F4 human IgG4 exp pC3AP313 anti-teta

## ALIGNMENTS

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Query Match 100.0%; Score 750; DB 1; Length 750; Best Local Similarity 100.0%; Pred. No. 1.8e-177; Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps	P-PSDB, R7611.  Treating glomerulonephritis with antibody against complement C5 component - to inhibit complement induced cell lysis Claim 38; Page 123-125; 181pp; English.  A DNA construct (T08483) codes for a humanised CDR-grafted and framework sequence-altered Fd 5G1.1 VH + IGHRL (R77610), which includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.  The DNA can be subcloned together with DNA (T08484) coding for a humanised light chain (R77612) into vector APEX-3P (T08476) for expression of humanised antibody in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular glomerulonephritis.  Sequence 750 BP; 163 A; 220 C; 197 G; 170 T;	Synthetic.  Synthetic.  Location/Qualifiers  cds	RESULT 1 108484 108484; Standard; DNA; 750 BP. 10 T08484; 11 T08484; 12 T08484; 13 T08484; 14 T08484; 15 T08484; 16 T08484; 17 T08484; 18 T08484; 19 T08484; 19 T08484; 10 T0848

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TGTAAAAGCTAGGGGCTATATTTTTTTATTATTGGATTCAATGGGTGCGTCAGGCCCCC
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Humanised 5G1.1 VH + IGHRLD DNA.
Complement C5; haemolysis; kidney; glomerulonephritis;
monoclonal antibody; antiinflammatory; antibody engineering;
humanised antibody; complementarity determining region; CDR;
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Thomas TC;
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01-MAY-1995; US-236208.
(ALEX-) ALEXION PHARM INC.
EVANS MJ, MALIS L, Mueller EE
Rother RP, Springhorn J P, Sq
Wang Y, Wilkins JA;
WPI; 95-392923760.
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            component - to inhibit complement induced cell lysis claim 37; Pages. 135-137; 181pp; English.

A DNA construct (108487) codes for a humanised CDR-grafted
light chain, designated 5G1.0 V + IGHRLD (R77615), which includes
CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The
DNA can be subcloned together with DNA (T08484) coding
for a humanised R(R77611) into vector APBX-3P (T08476) for
expression of humanised antibody in human 293 EBNA cells. Such
recombinant antibodies retain the ability of MAb 5G1.1 to block
human complement C5a generation and thus to reduce glomerular
inflammation and kidney dysfunction associated with
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glomerulonephritis with antibody against
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CA DNA construct (T08483) codes for a humanised CDR-grafted and C framework sequence-altered Fd SG1.1 VH + IGHRL (R77610), which includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.

CThe DNA can be subcloned together with DNA (T08484) coding for a humanised light chain (R77612) into vector APEX-3P (T08476) for expression of humanised antibody in human 293 EBNA cells. Such C expression of humanised antibody in human 293 EBNA cells. Such crecombinant antibodies retain the ability of MAD 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with Sc Johnson complement Say generation and thus to reduce glomerular C glomerulonephritis.

SQ Sequence 750 BP; 159 A; 225 C; 199 G; 167 T;
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Best Loc
Matches
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P-PSDB; R77610.
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Humanised 5G1.1 VH + IGHRL DNA.
Complement C5; haemolysis; kidney; glomerulonephritis;
monoclonal antibody; antiinflammatory; antibody engineering;
humanised antibody; complementarity determining region; CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-NOV-1995.
01-MAY-1995; U05688.
02-MAY-1994; US-236208.
(ALEX-) ALEXION PHARM INC.
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15-MAR-1996
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mes 737; Conserv
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98.3%;
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Pred. No. 2.6e
0; Mismatches
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Treating glomerulonephritis with antibody against complement C5 component to inhibit complement induced cell lysis Claim 26; Page 116-119; 181p9; English.

A DNA construct (708481) codes for chimeric light chain 5G1.1M1 VL HuK (R77608), which can form the light chain portion of an Fab.

The chimeric light chain includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The DNA can be subcloned with DNA (708482) coding for chimeric Fd (R77609) into vector APEX-3P (T08476) for prodn. of chimeric Fab in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis.

Sequence 750 BP; 174 A; 226 C; 191 G; 159 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric heavy chain 5G1.IM1 VL HuG1 DNA.

Complement C5; haemolysis; kidney; glomerulonephritis; monoclonal antibody; antiinflammatory; antibody engineering; humanised antibody; complementarity determining region; CDR;
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T08482;
02-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                  (ALEX-) ALEXION PHARM INC.
Evans MJ, Matls L, Mueller EE, Nye SH,
Rother RP, Springhorn J P, Squinto SP,
Wang Y, Wilkins JA;
WPI; 95-392923/50.
P-PSDB; R776609.
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01-MAY-1995; U05688.
02-MAY-1994; US-236208.
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Query Match Best Local Similarity

74.8%;

Score 561.2; DB 1; Pred. No. 1.3e-130;

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 Gaps
                 ATGAAGTGGAGCTGGGTTATTCTCTTCCTCCTGTCAGTAACTGCCGGCGTCCACTCCCAA 60
                                  ATGAAATGGAGCTGGGTTATTCTCTTCCTCTCTCAGTAACTGCAGGTGTCCACTCCCAG 60
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HFE7A, monoclonal antibody; mouse; Fas; humanised antibody;
apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
systemic lupus erythematosus; graft versus host disease;
Sjogren syndrome; pernicious anaemia; Addison's disease;
scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
rheumatoid arthritis; autoimmune haemolytic anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy; ds.
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Mismatches 118; Indels
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(SANY ) SANKYO CO LTD.

Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I, Masahiko O, Nobufusa S, Shin Y, Tohru T; P-PSDB; W83037.
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Location/Qualifiers
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                                                              /codon_start=
736. .1126
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/*tag= f
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08-OCT-1997; JP-276064.
01-APR-1997; JP-082953.
25-JUN-1997; JP-169088.
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Local

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DE Anti-IL-8 humanised antibody plasmid p6G4V11N35A.choSD.9. a
Humanised antibody; chimeric antibody; monoclonal antibody; mouse;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW dermattis; meningitis; encephalitis; uveitis; autoimmune disease;
KW rheumatoid arthritis; 5orgen's syndrome; vasculitis;
KW rauma; alcoholic hepatitis; promomia; pleurisy; alveolitis;
KW vasculitis; bronchitis; bronchitetasis; cystic fibrosis; diagnosis;
KW vasculitis; bronchitis; bronchitetasis; cystic fibrosis; diagnosis;
Chimeric - Homo saplens.
Key Chimeric - Homo saplens.
Location/Qualifiers
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CC encoding a humanised 664VIN35A IgG (see W69316) containing complementarity determining regions of murine anti-interleukin-8 CC (IL-8) monoclonal antibody (MAD) 665.2.5 (see W69309-10) in a CC human template. The plasmid has a pSVI backbone. Humanised CC anti-IL-8 MADs (see W69301-04) are described for use in diagnostic capplications and in the treatment of inflammatory disorders. The CC applications and in the treatment of inflammatory disorders. The CC dischemic reperfusion, adult responses associated with inflammatory to swel disease (such as Crohn's disease and ulcerative colitis), cc dischemic reperfusion, adult respiratory distress syndrome, vasculitis, meningitis, encephalitis, uveitis, autoimmune diseases such as rheumatoid arthritis, Sjorgen's syndrome, vasculitis, capticaemia or trauma, alcoholic hepatitis, bacterial pneumonia, cc chronic bronchitis, bronchiectasis, and cystic fibrosis.

Sequence 8120 BP; 2023 A; 2182 C; 1958 G; 1957 T;
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Best Local S
Matches 587
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27-AUG-1998.
20-FEB-1998; U03337.
22-JAN-1998; US-012116.
21-FEB-1997; US-804444.
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P-PSDB; W69316.
New conjugates of antibody
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TCGGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCT
                             AGCGCCTCCAACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCCTCCTCCAAGAGCACCTCT
                                                              CGCTACAATGGTGACTGGTTCTTCGACGTCTGGGGTCAAGGAACCCTTGGTCACCGTCTCC
                                                                              GGTTCTAGCCCGAATTGGTATTTTGATGTTTTGGGGTCAAGGAACCCTGGTCACTGTCTCG
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                                                                                                      Anti-Fas humanised antibody HFE7A heavy chain DNA.

Anti-Fas humanised antibody, mouse; Fas; humanised antibody;

HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;

M apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;

Systemic lupus erythematosus; graft versus host disease;

Systemic lupus erythematosus; graft versus host disease;

Systemic lupus erythematosus; graft versus host disease;

Socroderma; Goodpasture syndrome; Crohn's disease;

W rheumatoid arthritis; autoimmune haemolytic anaemia;

M myasthenia gravis; multiple sclerosis; Basedow's disease;

Athrombopenia purpura; insulin-dependent diabetes; allergy;

Alomopenia nephritis; hypoplastic anaemia; hepatitis; AIDS;

Homo sapiens.
       GGGGGCACAGCGGCCCTGGCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTG
                                                                       TCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG
                                       TCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC
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New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AlDS Claim 27; Page 210-212; 292pp; English.

Fig. myocarditis, hepatitis and AlDS Claim 27; Page 210-212; 292pp; English.

This nucleotide sequence codes for the VD type humanised heavy claim (see W83036) of murine anti-human Fas monoclonal antibody HFE7A. It was constructed from DNA fragments obtained by PCR CC Chain (see W83036) of murine anti-human Fas monoclonal antibody HFE7A. It was constructed from DNA fragments obtained by PCR CC Chain (see W83036) of murine anomonic DNA. Host coll Escherichia coli pgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion fragment of the humanised VPF HFE7A have coll Escherichia coli pgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion cording humanised antibodies by culturing host cells. Humanised versions of HFE7A (see W83031-37), like native HFE7A, are capable of inducing apoptosis in normal cells expressing Fas, and of colinguals apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of disease, that involve FasyFas ligand interactions, and also to collupus erythematosus, Hashimoto's disease, graft versus host disease, solarone, solarone, crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, rheumatoid arthritis, myasthenia dravis, myclinder anaemia, habritis, humania, habritis, and transplant rejection (all claimed). As and transplant rejection (all claimed). As and channed and channed and transplant rejection (all claimed).
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Best Local Similarity 81.1%; Pred. No. 1.2e-112;
Matches 582; Conservative 0; Mismatches 133;
25-JUN-1997; JP-169088.

(SANY ) SANKYO CO LTD.

Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa Masahiko O, Nobufusa S, Shin Y, Tohru T; P-PSDB; W8036.
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The wonjugates of antibody fragments - having covalently attached in the conjugates of antibody fragments - having covalently attached in the conjugates of antibody fragments - having covalently polyethylene if glycol, for improving the residence time in the circulation.

Example T; Fig 53; 328pp; English.

Cantibody 664.2.5VILN35A Fab' heavy chain (see W69304) modified to contain a Cys residue in the hinge region, and which contains the complementarity determining regions (CDRs) of murine anti-IL-8 concolonal antibodies Chain (see W69303). Humanised anti-IL-8 monoclonal antibodies (MAbs) and variants are described for use in diagnostic applications CC and in the treatment of inflammatory disorders. The invention CC provides conjugates of an antibody fragment and a non-proteinaceous polymer, such as PEG, that have improved half-life, mean residence time, and/or clearance rate compared to non-derivatised parental CC antibody fragment also claimed is a Rab' or Fab-SH antibody CC amino acids +1-233 of the heavy chain maino acid sequence composed of CC amino acids +1-233 of the heavy chain polypeptide of 664.2.5VIIN35A
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15-FEB-1999 (first entry)
15-FEB-1999 (first entry)
15-FEB-1999 (first entry)
164.2.5: Inflammation; immunotherapy; rab; interleukin-8;
164.2.5: Inflammation; immunotherapy; therapy; psoriasis;
1654.2.5: Inflammation; immunotherapy; therapy; psoriasis;
1654.2.5: Inflammation; adult respiratory distress syndrome;
1654.2.5: Inflammatory bowel disease; Crohn's disease; ulcerative colitis;
1654.2.5: Inflammatory bowel disease; Crohn's disease; useritis; municipalitis; encephalitis; uveitis; autoimmune disease;
1654.2.5: Inflammatory bowel disease;
1655.2.5: Inflammatory bowel disease;
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20-FEB-1998;
22-JAN-1998;
21-FEB-1997;
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Hsei V, Koumenis I, L
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Sequence 801 MP; 176 A; 235 C; 204 G; 186 T;
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new conjugates or antibody fragments - naving covalently attached non-proteinaceous or antibody fragments - naving covalently attached placely. For improving the residence time in the circulation. Disclosure; Fig 37: 328pp; English.

This DNA sequence encodes humanised anti-interleukin-8 (IL-8) antibody 664.2. SVININ35A heavy chain (see W65030) in an N-terminal fusion with the STII leader peptide and in a C-terminal fusion with the STII leader peptide and in a C-terminal fusion with the STII leader peptide and the conclains the complementarity determining regions (CDRs) of murine anti-IL-8 monoclonal antibodies (MADS) chain template. Humanised anti-IL-8 monoclonal antibodies (MADS) and in the treatment of inflammatory disorders. The invention provides conjugates of an antibody fragment and a non-proteinaceus of un the treatment of inflammatory disorders. The invention provides conjugates of an antibody fragment and an orderivatised parental antibody fragment. Also claimed are a polypeptide that is an antibody fragment. Also claimed are a polypeptide that is an antibody fragment antibody fragment comprising a light chain amino acid sequence comprising the light chain CDRs of 64.2.5711N35A (see W69301) or 664.2.5711N35A, in which the Cys231 and Cys231 and Cys231 and Cys231 and Sequence of 64.2.5711N35A in which the Cys231 and Cys231 and ulcerative colitis), ischemic reperfusion, adult respiratory distress syndrome, dermatitis, meningitis, encephalitis, userial support of 64.2.5711N35A in which the Cys231 and ulcerative colitis), ischemic reperfusion, and ulcerative colitis, diseases involving leukocyte dispeases; central nervous system inflammatory disorder, multippe organ injury syndrome, vasculitis, diseases involving leukocyte dispeases included cystic fibrosis. They can also be used in diagnostic applications. Syndrome eccondary to septicement and supplemental and some prop
                                                                           Humanised anti-IL-8 6G4.2.5V11N35A heavy chain DNA.

Humanised anti-IL-8 6G4.2.5V11N35A heavy chain DNA.

Humanised anti-IL-8 6G4.2.5V11N35A heavy chain DNA.

Humanised antibody; monoclonal antibody; interleukin-8;

GG4.2.5; inflammation; immunotherapy; therapy; psoriasis;

inflammatory bowel disease; Crohn's disease; ulcerative colitis;

dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;

rheumatoid arthritis; Sjorgen's syndrome; vasculitis;

reauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;

vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 98-467563/40.
P-PSDB; W69303.
New conjugates of antibody fragments - having covalently attached
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Hsei V, Koumenis I, Leong SR, Presta LR, Shahrokh 2,
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
31. 927
/*tag- a
31. 99
/*tag- b
/*tag- b
/*tag- x
100. -924
/*tag- c
                                       V55072 standard; DNA; 927
                                                                                                                                                                                                                                                                                                                                             Chimeric - Homo sapiens.
Chimeric - Mus sp.
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US-804444.
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21-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                               81 CGCCGAGGTCAAGAAGCCAGGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGGCTATAT 140
                                                                                                                                                                                    123 GGTGGCCTGGTGCAGCGGGGCTCACTCCGTTTGTCCTGTGCAGCTTCTGGCTACTC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 GGAGGACACGGCCGTCTATTATTGCGCGCGTTATTTTTTGGTTCTAGCCCGAATTGGTA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 TGAGGACACTGCCGTCTATTACTGTGCAAGAGGGGATTATCGCTACAATGGTGACTGGTT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381 TITIGATGTTTGGGGTCAAGGAACCCTGGTCACTGTCTCGAGCGCCTCCAACGGGCCC 440
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                                                                                                                      63 TATGTICGITTITCTATIGCTACAAACGCGTACGCTGAGGITCAGCTAGTGCAGTCTGG 122
                                           Gaps
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Anti-IL-8 humanised antibody plasmid p6G4V11N35A.F(ab')2.
Humanised antibody: chimeric antibody; monoclonal antibody; mouse;
Humanised antibody: chimeric antibody; mouse;
Humanised antibody: chimeric antibody; mouse;
inflammatory bowel disease; crohn's disease; ulcerative colitis;
ischaemic reperfusion; adult respiratory distress syndrome;
dermatitis; meningitis; encephalitis; uveritis; autoimmune disease;
rheumatorid arthritis; Sjorgen's syndrome; vasculitis;
leukocyte diapedesis; multiple organ injury syndrome; septicaemia;
trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 TTTTTCTAATTATTGGATTCAATGGGTGCGTCAGGCCCCCGGGCAGGGCCTGGAATGGAT
                                                                                                                                                                                                                                                                                                                                  201 GGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGT
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                                                                               21 TCTCTTCCTCCTGTCAGTAACTGCCGGCGTCCACTCCCAAGTCCAACTGGTGCAATCCGG
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  Length 927;
                                      Indels
Score 488; DB 1; L
Pred. No. 1.9e-112;
0; Mismatches 150;
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Query Match 65.1%;
Best Local Similarity 79.4%;
Matches 578; Conservative
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PT glycol, for improving the residence time in the circulation.

Example K; Fig 41A-U; 328pp; English.

CC This is the DNA sequence of vector plasmid p6G4V1IN35A.F(ab')2

CC encoding a murine-human chimeric Fab (see W69313) containing

CC (II-8) monoclonal antibody (MAb) 6G5.2.5 (see W69319-10) in a

CC human template. Humanised anti-II-8 MAbs (see W69309-10) in a

CC described for use in diagnostic applications and in the treatment

CC of inflammatory disorders. The invention provides conjugates of an

CC antibody fragment and a polymer, such as PEG, that have improved

CC conjugates can be used for immune therapy of e.g. psoriasis,

CC responses associated with inflammatory bowel disease (such as

CC conn's disease and ulcerative colitis), ischemic reperfusion,

CC adult respiratory distress syndrome, dermatitis, meningitis,

CC arthritis, Sjorgen's syndrome, vasculitis, diseases involving

CC arthritis, Sjorgen's syndrome secondary to septicaemia or trauma,

CC multiple organ injury syndrome secondary to septicaemia or trauma,

CC alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex

CC monochiectasis, and cystic fibrosis.

SQ Sequence 6563 BP; 1537 A; 1790 C; 1675 G; 1561 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9837200-A2.
27-AUG-1998.
20-FEB-1998; UO3337.
22-JAN-1998; US-012116.
21-FEB-1997; US-804444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1281
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Hsei V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;
therapy; p6G4V11N35A.F(ab')2; ds.
Chimeric - Mus sp.
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P-PSDB; W69313.
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                         GGAGGACACGGCCGTCTATTATTGCGCGCGTTATTTTTTTGGTTCTAGCCCGAATTGGTA
                                                                                                                                   TACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCTCCAGCCTGCGATC
                                                                                                                                                                                                                                                                                                   CTTCTCGAGTCACTATATGCACTGGGTCCGTCAGGCCCCGGGTAAGGGCCTGGAATGGGT
                                                                                                                                                                                                                                                                                                                                                      TTTTTCTAATTATTGGATTCAATGGGTGCGTCAGGCCCCCGGGCAGGGCCTGGAATGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCCGAGGTCAAGAAGCCAGGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGCTATAT
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TGAGGACACTGCCGTCTATTACTGTGCAAGAGGGGATTATCGCTACAATGGTGACTGGTT
                                                                                                                                                                                                   TGGATATTGATCCTTCCAATGGTGAAACTACGTATAATCAAAAGTTCAAGGGCCGTTT
                                                                                                                                                                                                                                                  GGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGT
                                                                                                                                                                                                                                                                                                                                                                                                     CGGTGGCCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCCTGTGCAGCTTCTGGCTACTC
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439. .1167
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79.4%;
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Pred. No. 3.2e-112;
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    having covalently attached
particularly polyethylene
time in the circulation.

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            PT New antibody 485 polynucleotides and polypeptides - used to develop PT products for the diagnosis and treatment of cancers and for products for the reduce risk of recurrence PT prophylactic therapy to recombinant human reduced the region (see W88464) of the recombinant human reduced reduced reduced reduced the recombinant human reduced red
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Monoclonal antibody 4B5 heavy chain variable region DNA.
Antigen binding fragment 4B5; monoclonal antibody; cancer;
neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma;
sarcoma; lung carcinoma; metastasis; anti-idiotype antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X06951 standard; DNA; 1449
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08-JUL-1997;
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                                                               adenocarcinoma, and liver metastases, hepatoma, cholangiocarcinoma, breast tumours such as ductal and lobular adenocarcinoma, squamous and adenocarcinomas of the uterine cervix, uterine and ovarian
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                                                                                                    epithelial carcinoma, prostatic adenocarcinoma, transitional squamous cell carcinoma of the bladder, B and T cell lymphoma (nodular and diffuse), plasmacytoma, acute and chronic leukemia, malignant melanoma, soft tissue sarcoma and leiomyosarcoma. Sequence 1449 BP. 342 A; 457 C; 398 G; 252 T;
                                                                                                                                                                                                                         15;
                                                                                                                                                                                                Length 1449;
invention can be used in the detection and treatment of e.g. astrocytoma, oligodendroglioma, ependymoma, medulloblastoma, primitive neural ectodermal tumour (PNET), pancreatic ductal adenocarionma, small and large cell lung adenocarcinomas, squamous cell carcinoma, bronchoalveoarcarcinoma, epithelial
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78.8%; Pred. No. 2.4e-112;
iive 0; Mismatches 147;
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New antibody 4B5 polynucleotides and polypeptides - used to develop products for the diagnosis and treatment of cancers and for products for the diagnosis and treatment of cancers and for products for the diagnosis and treatment of cancers and for Claim 6; Page 7B; 8B9P; English.

This is the complementary strand of a DNA sequence (see also This is the complementary strand of a DNA sequence (see also This is the complementary strand of a DNA sequence (see also This is the recombinant human monoclonal antibody (MAD) 4B5. 4B5 of the recombinant human monoclonal antibody (MAD) 4B5. 4B5 of the recombinant human monoclonal antibody (MAD) 4B5. 4B5 recognises antibodies specific for GD2 antigen antibodies. Such neuroblastoma, malignant and/or metastatic melanoma, breast colon adenocarcinoma, unique and prostate adenocarcinoma, breast colon adenocarcinoma, breast and prostate adenocarcinoma. The invention encompasses 4B5 derivatives with immunologic specificity for netiodies specific for GD2. These derivatives, or antigen binding fragments, may comprise regions of these 4B5 VD3 function and regions spanning the 4B5 CDRs. Other derivatives include Fab, F(ab/)2, comprising the 4B5 CDRs. Other derivatives include Fab, F(ab/)2, comprising these polynucleotides. 4B5 mincs GD2, and is useful in generating a host immune response to cancer. Products of the treatment of enguarention can be used in the detection and treatment of enguarention can be used in the detection and treatment of enguarention can be used in the detection and treatment of enguarentions. Small and large cell lung adenocarcinoma, small and large cell lung adenocarcinoma, and liver metastases, hepatoma, childing and denocarcinoma, and liver metastases, hepatoma, collangiocarcinoma, small and lobular adenocarcinoma, and liver metastases, hepatoma, collangiocarcinoma, small and large cell lung denocarcinoma, and liver metastases, hepatoma, collangiocarcinoma, and denocarcinoma, and diffuse). Plasmate adenocarcinoma, and diffuse) plasmate adenocarcinoma, and dif
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                                                                          10-MAY-1999 (first entry)
Monoclonal antibody 4B5 heavy chain variable region DNA.
Antigen binding fragment 4B5; monoclonal antibody; cancer;
neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma;
sarcoma; lung carcinoma; metastasis; anti-idiotype antibody;
GD2 antigen; human; ds.
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                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers complement (1. .1431)
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standard; DNA; 1449 BP
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WPI; 99-120769/10.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1011
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/*tag- g
/label- FR3
386. .439
                                                                                /*tag= f
/label= CDR2
290. .385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= e
/label= FR2
239. .289
                                                                                                                                                                                                                                                                                                                                                                            /*tag= c
/label= FR1
182. .196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 35. .1465
                                                                                                                                                                                                                                                                               /label= CDR1
197. .238
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cDNA library;
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positive; patient;
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kappa; L;
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Best Loc
Matches
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14-JUL-1992;
15-JUL-1991;
15-JUG-1991;
01-AUG-1991;
23-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2; 35pp; English.

The sequences given in Q35099:100 encode the heavy and light chains of Antibody D respectively. Antibody D is a monoclonal antibody which was derived from peripheral blood lymphocytes from a hepatitis A virus (HAV) sero positive patient. Antibody D is closely related in nature to murine antibody B5B3. Total RNA was solated from antibody Expressing cells and polyadenylated RNA was extracted. These polyA RNA's were used to prepare a cDNA library which was screened for human kappa light (L) chains and two positive clones were detected.

Further heavy (H) chain clones were also isolated.

Sequence 1617 BP; 375 A; 526 C; 441 G; 275 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodn. of recombinant primate antibodies - useful for treatinfections caused by hepatitis A, B and C, herpes, cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 93-019951/03.
P-PSDB; R31024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crowe JS, Lewis AP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arthritis etc.
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Local Similarity
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           GAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATG
                                                                                                                GGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACC
                                                                                                                                                                                                                       GTCCAACTGGTGCAATCCGGGGCCGAGGTCAAGAGCCAGGGGCCTCAGTCAAAGTGTCC
                                                                                                                                                                                                                                                                        ATGAAGTGGAGCTGGGTTATTCTCTTCCTCCTGTCAGTAACTGCCGGCGTCCACTCCCAA
                                                                                                                                                                                                       ATGCAGGTGGTGCAGTCTGGGGCTGAAGTAAAGAAGCCTGGGTCCTCGGTGACGGTCTCC
                                                                                                                                                                                                                                                         ATGGACTGGACCTGGAGGTTCCTCTTTGTGGTGGCAGCAGCTACAGGTGTCCAGTCCCAG
GAGCTGACTAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGACAGATCGCTAC
                                                 CAGAACTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACCAGCACAGCCCACATG
                                                                                                                                                                             TGTAAAGCTAGCGGCTATATTTTTTCTAATTATTGGATTCAATGGGTGCGTCAGGCCCCC
                                                                                                   GGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTCTTTTTGGTACACCAACCTACTCA
                                                                                                                                                      TGCAAGGCATCTGGAGGCACCTTCAGCAACTATGCTATCAGCTGGGTGCGACAGGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 306420.
; GB-015284.
; GB-016594.
; GB-006284.
                                                                                                                                                                                                                                                                                                            Conservative
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/label= CDR3
440. .472
440= i
/*tag= i
/label= FR4
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/label= CH2
1142 .1462
/*tag= m
/label= CH3
1566 .1571
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764. .811
/*tag= k
/label= HINGE
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473. 763
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The sequence shows a vector contg. TCAEB, a gene encoding a chimeric anti-CDO antibody for treatment of B cell lymphomas. TCAEB contains 4 transcriptional cassettes, human Ig 11ght and heavy chain constant regions, dihydrofolate reductase, neomycin phosphotransferase and murine variable regions. The vector can be used to produce antibodies which cause depletion of peripheral blood B cells, including those associated with lymphoma. They mediate complement-dependent lysis and lyse target cells by antibody-dependent cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2400 AFGGGTFGGAGCCTCATCTTGCTTGTCGCTGTTGCTACGCGTGTCCTGTCCCAG 2459
                                                                                                                       TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCC 525
                                                                                                                                                                                           645
                                                                                                                                                                                                                                                                                        646 AGCITGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 705
                                                                                                                                                                                                                                                                                                       Gaps
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            ----TTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAACC
                                      AGGCAGGCAAATTTTGACCGGGCCCGGGTTGGCTGGTTCGACCCCTGGGGCCAGGGCACC
                                                                                CTGGTCACTGTCTCGAGCGCCTCCACCAAGGCCCCATCGGTCTTCCCCCTGGCGCCTTCC
                                                                                                                                                 515 TCCAAGAGCACCTCTGGGGGCACAGCGGCCTGGGCTGCTGGTCAAGGACTACTTCCCC
                                                                                                                                                                              GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACCTTCCCC
                                                                                                                                                                                                                                   GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (first entry)
Vector contg. TCAE 8 DNA.
B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
cell lysis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.5%; Score 476; DB 1; Length 9208; 78.2%; Pred. No. 3.3e-109; ive 0; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                              706 GACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACAT 748
                                                                                                                                                                                                                                                                                                                                                            2388 G;
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Hanna N,
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12-NOV-1993; U10953.
13-NOV-1992; US-978891.
03-NOV-1993; US-149099
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See also Q65629-35.
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Best Local Similarity
Matches 585; Conserv
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Anderson DR,
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Traget plasmid Molly containing anti-CD20 gene.

Molly: target plasmid; gene integration; gene amplification;

Chimeric - Mus sp.

Chimeric - Escherichia coli.

Chimeric - Escherichia coli.

Chimeric - Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2997 TCAGGACTCTACTCCCTCAGCAGCGTGGTGCCCTCCAGCAGCTTGGGCACCAG
2460 GTACAACTGCAGCAGCCTGGGGCTGAGCTGTGAGCCTGGGGCCTCAGTGAAGTGTCC
                                                                                                 181 GGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACC
                                                                                                                                                                                              2640 CAGAAGTICAAAGGCAAGGCCACATIGACTGCAGACAAATCCTCCAGCACAGACCTACATG
                                                                                                                                                                                                                                                                                                                                                            301 GAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGCGCGCGTTATTTTTT
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                                                                      121 TGTAAAGCTAGCGGCTATATTTTTTTTAATTATTGGATTCAATGGGTGCGTCAGGCCCCC
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361.363
/*tag= a
/note= "these bases represent nucleotides
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Chimeric - Photinus sp.
Chimeric - Salmonella typhimurium.
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"these bases represent nucleotides missing from the sequence given in the specification. They are included to maintain the nucleotide numbering in the specification for this sequence" 8522  k "these bases represent nucleotides missing from the sequence given in the specification. They are included to maintain the nucleotide numbering in the specification for this sequence."	this base represents a nucleotide missing from the sequence given in the specification. It is included to maintain the nucleotide numbering in the specification for this sequence"  if this base represents a nucleotide missing from the sequence given in the specification. It is included to maintain the nucleotide numbering in the specification for this sequence"  if the sequence given in the sequence given in the sequence given in the specification. It is included to maintain the nucleotide numbering in the specification for this sequence.	these bases represent nucleotides missing from the sequence given in the specification. They are included to maintain the nucleotide numbering in the specification for this sequence"  g this base represents a nucleotide missing the sequence given in the specification. It is included to maintain the nucleotide numbering in the specification for this sequence"  h	"this base represents a nucleotide missing from the sequence given in the specification. It is included to maintain the nucleotide numbering in the specification for this sequence"  "these bases represent nucleotides missing from the sequence given in the specification. They are included to maintain the nucleotide numbering in the specification for this sequence"	specification for this sequence"  b  these bases represent nucleotides missing from the sequence given in the specification. They are included to maintain the nucleotide numbering in the specification for this sequence"  c  this base represents a nucleotide missing from the sequence given in the specification. It is included to maintain the nucleotide numbering in the specification for this sequence"
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HARM CORI Lachlan I /44. integrati s - comp ks - and the 8; 114pp cleotide cludes the erichia c e comprise s and SV ydrogenas	18901 /*tag- /note- /note- US-023715. US-023715.	16321 /*tag- /note- /18541 /*tag- /note-	13381. /*tag= ./note= ./note= 15961. /*tag= /note=	/note- 12061 /*tag- /note- 12421 /*tag- /note-
(IDEC-) IDEC PHARM CORP.  Barnett RS, McLachlan KR, Reff ME; WPI; 98-52129/44.  Site specific integration of DNA in mammals for expressing, e.g. Site specific integration of DNA in mammals for expressing, e.g. immunoglobulins - comprises homologous recombination using selectable marker and target plasmids.  Example 1; Fig 8; 114pp; English.  This is the nucleotide sequence of novel target plasmid Molly. This is the nucleotide sequence of novel target plasmid Molly. The plasmid includes the murine dihydrofolate reductase (DHFR) gene, the Escherichia coli beta-galactosidase gene, baculovirus DNA, a cassette comprising the promoter and enhancer elements from cytomegalovirus and SV40 virus, the E. coli beta-glucuronidase (GUS) gene, firefly luciferase gene, Salmonella typhimurium histidinol dehydrogenase gene (HisD) and transposon Tn5 neomycin	intain the nu crification for scification for sequenom the sequenom crification.	specification. The maintain the nucleo specification for 1 q this base represent from the sequence specification. It maintain the nucleo specification for 1 r this base represent from the sequence cancel finance of the sequence of the seq	a · a ·	

phosphotransferase (neo) gene sequences, in a pBR-derived backbone, and allos an anti-B cell antigen CD20 chimeric antibody C2BB gene.

The invention provides a novel method for integrating a desired exogneous DNA at a target site within the genome of a mammalian cell with a homologous recombination. This involves transfecting the cell with a 'marker plasmid' such as Desmond (see V61792), which contains a unique sequence that is foreign to the mammalian cell genome and which provides a substrate for homologous recombination, to Mandy (see V6174), containing a sequence which provides for or Mandy (see V6174), containing a sequence which provides for composing plasmid, and further comprising a desired DNA that is composited into the mammalian cells, typically an immunoglobulin or other secreted mammalian glycoprotein. The homologous recombination system utilises the neo gene as a dominant selectable marker. The neo gene is split into 3 exons. Exon 3 is present on the marker plasmid and becomes integrated on the marker plasmid and becomes integrated on the marker plasmid and becomes integrated on the marker plasmid and see separated by an intron into which at conto the mammalian cells. Exons 1 and 2 are present on the marker plasmid and are separated by an intron into which at the targeting plasmid, and are separated by an intron into which at the correct splicing of all 3 exons of the neo gene and expression of the targeting vector with the integrated marking vector results of a functional neo protein. The method is applicable to all protein. The use of a triply spliced selectable marker means that all selected colonies arise from homologous recombination. In protein, the number of colonies that need to be screened to identify high producer clones is reduced. An amplifiable gene completed to this site, the gene is further enhanced by gene is targeted to this site, the gene is further enhanced by gene is further enhanced.

Query Match 63.5%; Score 476; DB 1; Length 19001; Best Local Similarity 78.2%; Pred. No. 3.9e-109; Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps

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 Db 9606 GGTCGGGGCCTGGAATGGATTGGAGCTATTTATCCCGGAAATGGTAATTCTCTACAAT 9665
Qy 241 GAAAATTTTAAAGACCGTGTTACTACGTGACACTTCGACTACTATGATG 300

GGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACC 240

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US-08-189-575-159
US-08-1899-575-159
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29,	Sequence 29, Appl	Sequence 29, Appl	•	ω '	Sequence 3, Appli		Sequence 1, Appli	Sequence 1, Appli	•		Sequence 2, Appli	`	•	•	Sequence 57, Appl	•	•	Sequence 57, Appl

ALIGNMENTS

## PRIOR APPLICATION UNMBER: 60/038, DOWN APPLICATION NUMBER: 60/038, DOWN APPLICATION NUMBER: 21-Feb-1997 ATTORNEY/ACENT INFORMATION: NAME: LOVE, RICHARD B. REGISTRATION NUMBER: 34,659 REFERENCE/DOCKET NUMBER: P1085 TELECOMMUNICATION INFORMATION: TELEPHAX: 650/225-5530 TELEPHAX: 650/952-9881 INFORMATION FOR SEQ ID NO: 68: SEQUENCE CHARACTERISTICS: LENGTH: 8120 base pairs TYDE: Nucleic Acid STRANDEDNESS: Single TOPOLOGY: Linear US-09-027-449-68 Patent No. 6025158 PATENT NO. 6025158 GENERAL INFORMATION: APPLICANT: Genzalez, Tania R. APPLICANT: Leong, Steven R. APPLICANT: Presta, Leonard G. TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibo RESULT 1 US-09-027-449-68 Sequence 68, COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION UMBER: 60/074,330 FILING DATE: 22-Jan-1998 PRIOR APPLICATION DATA: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS CITY: South San FI STATE: California COUNTRY: USA APPLICATION NUMBER: US/00 FILING DATE: 20-Feb-1998 3, Application US/09027449 6025158 1 DNA Way Genentech, Francisco Humanized Anti-IL-8 Monoclonal Antibodies 72 US/09/027,449 P1085R3-2

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                                                                                                                                                                                                                                                                                                                                                                                                               421 AGGGCCTCCACCAAGGGCCCATGGGTCTTCCCCCTGGCGCCCTCCTCCTAAGAGCACCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 69, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                           ;
0
 Length 8120;
                           Indels
  Score 495.2; DB 5;
Pred. No. 5.7e-120;
                          0; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
66.0%;
78.9%;
                           Conservative
              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-09-027-449-69
               Best Local Sim
Matches 590;
  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 CGCCGAGGTCAAGAAGCCAGGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGCTATAT 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 TITITCTAATTATTGGATTCAATGGGTGCGTCAGGCCCCGGGCAGGGCCTGGAATGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 TACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCTCCAGCCTGCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 CACTTTATCTCGCGACAACTCCAAAAACACAGCATACCTGCAGATGAACAGCCTGCGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 recararatrerecriceargereaactaceraraarcaaagricaaggecerrr
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Pred. No. 2.2e-118;
0; Mismatches 150;
                              disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                            SOFTWARE: Winderin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION TOWNER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-197
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                         P1085R3-2
                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1C
TELECOMMUNICATION INFORMATION:
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79.4%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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Best Local Similarity 79.4
Matches 578; Conservative
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TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5

SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-027-449-59
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US-09-027-449-59
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GENERAL INFORMATION:
                                                                     Query Match
Best Local Similarity
Matches 578; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb fla
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Windratin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/074,330

FILING DATE: 22-Jan-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664

FILING DATE: 21-Feb-1997

ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: 91085R3

TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/027,449 FILING DATE: 20-Feb-1998 CLASSIFICATION: 435
     63
                                    21
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                      TCTCTTCCTCCTGTCAGTAACTGCCGGCGTCCACTCCCAAGTCCAACTGGTGCAATCCGG 80
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     TATGTTCGTTTTTTCTATTGCTACAAACGCGTACGCTGAGGTTCAGCTAGTGCAGTCTGG 122
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6025158
                                                                      Conservative
                                                                                      65.18;
79.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.44 Mb floppy
                                                                     0;
                                                                                                                                                                                                                                                                                                                              P1085R3-2
                                                                                      Score 488; DB 5;
Pred. No. 2.3e-118;
                                                                     Mismatches 150;
                                                                                                  Length 927
                                                                     Indels
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US-09-027-449-61
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                                                                                                                                                                                                      Patent No. 6025158

GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven G.
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibo
                                                                                                                                                                                                                                                                                                                                          Sequence 61,
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb 1
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
                                                                                                                  ADDRESSEE: Genented
STREET: 1 DNA Way
CITY: South San Fra
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189
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                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                           TCACACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAG 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTGATGTTTGGGGTCAAGGAACCCTGGTCACTGTCTCGAGGGCCCTCCACCAAGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGGACACGGCCGTCTATTATTGCGCGCGCTTATTTTTTGGTTCTAGCCCGAATTGGTA 380
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1 ATGAAGTGGAGCTGGGTTATTCTCTTCCTCTGTCAGTAACTGCCGGCGTCCACTCCCAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.8%; Score 478.2; DB 3;
78.0%; Pred. No. 9.4e-116;
iive 0; Mismatches 153;
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
                                                                                                                                                                                                                                                                                                                         STREET: SOTHWELL, FIGG, ERNST & KURZ STREET: 555 THIRTEENTH ST. N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 Dase Pairs
                                                                                                                                                                                                                     Sequence 9, Application US/08378939
Patent No. 5876961
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Matches 595; Conservative
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93..1465
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STRANDEDNESS: both
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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2001 TCACACAT 2008
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                                                                                          741 TCACACAT 748
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                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 20004
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FEATURE:
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COCATION:
US-08-378-939-9
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US-08-378-939-9
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Pred. No. 4e-118;
0; Mismatches 150; Indels
         APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan 1998
PRIOR APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
RECISTRATION NUMBER: 44,659
REFERENCE/DOCKET NUMBER: 91085R3-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 6563 base pairs
TYPE: NUCLEIC Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.1%;
Best Local Similarity 79.4%;
Matches 578; Conservative 0
CURRENT APPLICATION DATA:
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US-09-027-449-61
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                                                                                                                                                                Sequence 3, Application US/08149099C Patent No. 5736137 GENERAL INFORMATION:
                                                                                                                                      APPLICANT:
APPLICANT:
                                                    APPLICANT: LEONARD, John E.
APPLICANT: REFF, Mitchell E.
APPLICANT: REFF, Mitchell E.
APPLICANT: REFF, Mitchell E.
APPLICANT: RASTETTER, William H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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                                     E: BURNS, DOANE,
P.O. Box 1404
                                                                                                                                               HANNA, Nabil
                                                                                                                                                        ANDERSON,
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                                              SWECKER
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Query Match
Best Local S
Matches 585
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: .Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
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APPLICATION NUMBER: US 07/978,891
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DI
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Local Similarity 78.2%;
hes 585; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/149,099C FILING DATE: 03-NOV-1993 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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TCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACCACCTTCCCCGGCTGTCCTACAGTCC
                                                                                                                                        CAGAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATG
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(703) 836-2021
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Pred. No. 5.9e-115;
0; Mismatches 160;
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Query Match 63.5%;
Best Local Similarity 78.2%;
Matches 585; Conservative
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APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Reff. Mitchell E.
APPLICANT: Restetter, William H.
ITLE OF INVENTION: Therapeutic Application of Chimeric and
ITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell
ITLE OF INVENTION: Lymphoma
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
STRFFT:
STRFFT:
2938 TCGIGGAACTCAGGCGCCCTGACCAGCGGCGTGCACCTTCCCGGCTGTCCTACAGTCC 2997
                                                                                                         3058 ACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGCAGGAG 3117
                          ACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAG
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION UNBER: US/08/476,275
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION NUMBER: US 07/79,8,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
RESISTRATION NUMBER: 03-030
RESISTRATION NUMBER: 03-030
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TELEPHONE: 703-836-6620
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
FURTH: 9209 base pairs
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STRANDEDNESS: single
TOPOLOGY: circular
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Sequence 3, Application US/08478967A

Patent No. 5843439

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: HANNA, Nabil

APPLICANT: NEWMAN, ROLand A.

APPLICANT: REFF, Mitchell E.

APPLICANT: REFF, William H.

TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND

TITLE OF INVENTION: THERAPEUTIC APPLICATION ANTIGEN FOR THE TREATMENT OF B CELL

TITLE OF INVENTION: LYMPHOMA
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                                                            Gaps
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                                                         0; Mismatches 160;
Score 476; DB 2; 1
Pred. No. 5.9e-115;
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US-08-478-967A-3
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NUMBER OF SEQUENCES:

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Best Local S
Matches 585
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REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9209 base pairs
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APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/978,891
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOSY'N BORYATION:
2759
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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HYPOTHETICAL:
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                                                                                                                                       2641 CAGAAGTTCAAAGGCCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATG
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CITY: Alexandria
STATE: Virginia
COUNTRY: United S1
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STRANDEDNESS: single
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CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGAAGTGGAGCTGGGTTATTCTCTTCCTCCTGTCAGTAACTGCCGGCGTCCACTCCCAA 60
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                  GGTTCTAGCCCGAATTGGTATTTTGATGTTTTGGGGTCAAGGAACCCTGGTCACTGTCTCG 420
                                                                   CAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTT---
                                                                                    GAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATG 300
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P.O. Box 1404
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nilarity 78.2%;
Conservative
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Pred. No. 5.9e-115;
0; Mismatches 160;
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Query Match Best Local Similarity Matches 585; Conserv

Conservative

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63.5**%**; 78.2**%**;

Score 476; DB 3; Pred. No. 7.3e-115; Mismatches 160;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2,
Patent No.
                                                                                          TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/819,866 FILING DATE: 14-MAR-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT TITLE OF INVENTION: SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS TITLE OF INVENTION: RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                       NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Alexandria
STATE: Virginia
                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                             LENGTH:
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MCLACHLAN, Karen Retta
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O. Box 1404
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CORRESPONDENCE ADDRESS:
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                      9433 ATGGGTTGGAGCCTCATCTTGCTCTTCTTGTCGCTGTTGCTACGCGTGTCCTGTCCCAG 9492
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                                                 GICCAACTGGTGCAATCCGGCGCGGGGTCAAGAAGCCAGGGGCCTCAGTCAAAGTGTCC 120
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1 ATGAAGTGGAGCTGGGTTATTCTCTTCCTCCTGTCAGTAACTGCCGGCGTCCACTCCCAA
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CITY: Alexandria
STATE: Virgini-
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Patent No. 5998144
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
APPLICANT: BARNETT, Richard Spence
APPLICANT: MCLACHIAN, Karen Retta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 476; DB 4; Le
Pred. No. 7.3e-115;
0; Mismatches 160;
                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/819,866
FILING DATE: 14 - WAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, KOBİN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-352
TELECHONUNICATION INFORMATION:
TELEPKEN: (703) 836-6520
TELEPKX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18986 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-023-715-2
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Best Local Similarity 78.2%;
Matches 585; Conservative
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; NAME/KEY:
; LOCATION:
US-08-276-852-154
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US-08-276-852-154
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                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION UNMBER: US 07/954,148
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 154:
STOTTENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1:
Patent No.
                                      Query Match
Best Local Similarity
Matches 577; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 3282 base pairs
TYPE: nucleic acid
                                                                                                                                                                         FEATURE:
                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        721
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CITY: La Jolla STATE: CA COUNTRY: USA
                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: line
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ATGAAGTGGAGCTGGGTTATTCTCTTCCTCCTGTCAGTAACTGCCGGCGTCCACTCCCAA 60
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                                        Conservative
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                                                                                                                                                                                                       linear
                                                                                                                                                                                    DNA (genomic)
                                                                                                                                                                                                                      double
                                                       62.3%;
78.7%;
                                      0
                                                   Score 467.4;
Pred. No. 7.5
                                        Mismatches
                                    1; DB 1;
7.5e-113;
hes 141;
                                        Indels
                                                                    Length 3282;
                                      15;
                                    Gaps
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                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                               TITLE OF INVENTION: HUITITLE OF INVENTION: TO NUMBER OF SEQUENCES: 1'CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
COMPUTER READABLE FORM:
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          ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5652138th Torrey Pines Road, Suite STREET: Mail Drop TPC8 CITY: La Jolla STATE: CA COUNTRY: USA COUNTRY: USA ZIP: 92037
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                                                                                                                                                              HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
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2728 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACCTTCCCG 2669
                                                                 586 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Burton, Dennis R

APPLICANT: Burton, Carlos F

APPLICANT: Barbas, Carlos F

APPLICANT: Lerner, Richard A

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

ITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS

NUMBER OF SEQUENCES: 170

CORRESPONDERS: The Scripps Research Institute, Office of

ADDRESSEE: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,

STREET: Mail Drop TPC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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FILING DATE: 24-JUL-1997
CLASSIPICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
APPORNEY/AGENT INFORMATION:
NAME: FILLING, THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCR1452P
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 154, Application US/08899575 Patent No. 5770440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFRENCE/DOCKET NUMBER: SCRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 3282 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                       2548 GACAAGAAAGTTG 2536
                                                                                                                                                                                                                            706 GACAAGAAGTIG 718
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STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92037
                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-08-899-575-154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION:
US-08-899-575-154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACGGAATATACC 240
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              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 467.4; DB 1;
Pred. No. 7.5e-113;
0; Mismatches 141;
                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                       APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                        SCR1452P
                                                                                                                                                                                                                                                                                                                                      NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: DNA (genomic)
US-08-276-852-169
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Best Local Similarity 78.7%;
Matches 577; Conservative
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 3282 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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RESULT 14
US-08-899-575-169/c
Sequence 169, Appli
Patent NO. 5770440
GENERAL INFORMATIC
APPLICANT: BUIT
APPLICANT: BUIT
APPLICANT: HAPPLICANT: LOIT
TITLE OF INVENTI
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OUNBER OF SEQUEN
CORRESPONDENCE J
ADDRESSEE: PI
ADDRESSEE: PI
ADDRESSEE: PI
ADDRESSEE: MA11
CITY: LA JOI:
                                                                               Sequence 169, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN USBUTRALIZING MONOCLONAL A
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRU
NUMBER OF SEQUENCES: 170
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Matches
 NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Ins
ADDRESSEE: Patent Counsel
STREET: 1666 No. 5770440th Torrey
STREET: Mail Drop TPC8
CITY: La Jolla
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); Mismatches 141;
                                                        Institute,
                              Pines Road, Suite
                                                          Office
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; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 16
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3282 base pairs
TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic
US-08-899-575-169
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Best Local S
Matches 577
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FILING DATE: 24-7UL-197
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION WIMBER: US 08/276,852
PRIOR APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-7UL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 07/954,148
APPLICATION NUMBER: US 07/954,148
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COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PATENTIN Release #1.0, Ve
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577; Conserv
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78.7%;
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Pred. No. 7.5e-113;
0; Mismatches 141;
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; LOCATION:
US-08-899-575-154
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                                                                                                     466 TCCAAGAGCACCTCTGGGGGCACAGGGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
               526 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACATCCCG
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: TO HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCR1452P
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FILING DATE: 24-JUL-1997
                                                                                                                                                                                                                                                                                                      Sequence 154, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 3282 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fitting, Thomas REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                           2548 GACAAGAAGTIG 2536
                                                                                                                                                                                                             706 GACAAGAAGTIG 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
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AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 705
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                                                                                                                                             GTCCAACTGGTGCAATCCGGCGCGCGGGGTCAAGAAGCCAGGGGGCCTCAGTCAAAGTGTCC 120
                                                                                                                                                               Gaps
                                                                      1 ATGAAGTGGAGCTGGGTTATTCTCTTCCTCCTGTCAGTAACTGCCGGCGTCCACTCCCAA 60
                                                                                                         15 ATGGAATGGAGCTGGGTCTTTCTCTTCTTCCTGTCAGTAACTACAGGTGTCCACTCCCAG 74
                                                                                                                                                                                                                                               135 TGTCAGGCTTCTGGATACAGATTCAGTAACTTTGTTATTCATTGGGTGCGCCCAGGCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GGCCAGGCCTGGAATGGATGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACC
                                                                                                                                                                                                                                                                                                                                                             241 GAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGCGCG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406 CIGGICACTGICTCGAGGGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
 Length 3282;
                                     Indels
Score 467.4; DB 2;
Pred. No. 7.5e-113;
0; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: September 12, 2000, 20:38:29 Job time: 4706 sec
Query Match 62.3%;
Best Local Similarity 78.7%;
Matches 577; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACAAGAAAGTTG 718
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Page 13

5/7/18 (Item 18 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06105444 BIOSIS NO.: 000085068593

PREPARATION AND CHARACTERIZATION OF MONOCLONAL ANTIBODIES AGAINST THE FIFTH COMPONENT OF RABBIT COMPLEMENT C5

AUTHOR: GICLAS P C; BAKER S L; GILLESPIE M L; WILCOX C

AUTHOR ADDRESS: DEP. PEDIATR., NATL. JEW. CENT. IMMUNOL. RESPIR. MED., 1400

JACKSON ST., DENVER, COLO. 80206, USA.

JOURNAL: J IMMUNOL METHODS 105 (2). 1987. 201-210. FULL JOURNAL NAME: Journal of Immunological Methods

CODEN: JIMMB

RECORD TYPE: Abstract LANGUAGE: ENGLISH

ABSTRACT: By immunizing mice genetically deficient in C5 we were able to obtain a group of monoclonal antibodies to rabbit C5 that cross-react with C5 from a wide variety of mammalian sera, including mouse. The specificity of the monoclonal antibodies was against native C5 and C5b but not C5a. The antibodies strongly inhibit the expression of C5 hemolytic activity. We suggest that these monoclonal antibodies will be useful for studying C5 as well as providing a way to selectively deplete C5 from plasma in vitro or in vivo.